6.0 86827 3 PFMAL1P3 5.8 67970 3 PFMAL1P3 5.8 172816 9 AC093899 5.8 4601 3 DMU1584 5.8 15917 3 DMU37541 5.8 159618 9 AC096750	5.7 172724 2 AC098590 AC098590 Homo 5.7 159618 9 AC096750 AC096750 AC096750 Homo 5.6 168698 9 AC066138 Homo 5.6 168698 9 AC066138 Homo	5.5 349980 6 AX344555 AX344555 5.5 14867 3 AE001398 AE01398 5.5 104992 2 AC005504 AC005504 5.5 169546 2 AC004157 AC004157	5.5 104992 2 AC005504 AC005504 Plasm 5.5 169546 2 AC004157 AC004157 Plasm 5.5 155106 2 AC104069 HOMO	5.5 326924 2 AC093082 AC093082 Homo 5.5 181792 9 AC098822 AC098822 Homo 5.4 205130 2 AC105425 Homo	5.4 155106 2 AC104069 AC104069 Homo 5.4 246080 2 AC104073 AC104073 Homo 5.4 168698 9 AC068138 AC068138 AC068138 Homo 5.4 181792 9 AC098822 AC068128 Homo	5.3 172724 2 AC098590 AC098590 5.3 326924 2 AC093082 AC093082 5.3 130117 9 AC004907 AC004907 5.3 158398 2 AC011146 AC011146	5.3 14067 3 AE001398 5.3 205130 2 AC105425 5.3 86827 3 PFMAL3P5 5.2 349980 6 AX344555	5.2 136357 2 AL161942 AL161942 5.2 183584 9 AC012492 AC012492 5.2 137889 9 AC073269	5.2 15421 3 PFCOMPIRA X95275 P. 5.2 183584 9 AC012492 AC012492 5.1 101188 2 AC010606 AC010606	5.1 184838 9 ACC90740 ACC90740 HOMO E 5.1 152209 9 HS1108D11 AL034419 Human 5.1 153098 9 ACC006970 ACC006970 HOMO E 5.1 152209 9 HS1108D31 AV034416	5.1 136098 9 AC104073 5.1 135250 9 AC104320 AC10432 5.1 136098 9 AC006970 AC00697	ALIGNMENTS	FMALI3P5 B6827 bp DNA linear INV 04-MAY-2000 lasmodium falciparum MAL3P5, complete sequence. LOAKSEK ALOARGY1 A	ALO10206 ALO10210 AL139179 ALO14556.3 GI:7711064 HTG; centromere; CTRP protein; initiation factor E4;	Serine/threonine protein phosphatase. malaria parasite P. falciparum. Plasanodium falciparum	<pre>backaryota, Arvectated Aptromptexa; Haemosporida; Plasmodium. backaryota, Arvectated Aptromptexa; Hosses 1 to 86827) Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T., Churcher,C.W., Cralg,A., Davies,R.M., Devlin,K., Feltwell,T., Gentles,S., Gwilliam,R., Hamilin,N., Harris,D., Holroyd,S., Hornoby,T., Horrocks,P., Jagels,K., Jassal,B., Kyes,S., McLean,J.,</pre>	Moule,S., Mungall,K., Murphy,L., Oliver,K., Quail,M.A., Rajandream,MA., Rutter,S., Skelton,J., Squares,R., Squares,S., Sulston,J.E., Whitehead,S., Woodward,J.R., Newbold,C. and Barrell,B.G. The complete nucleotide sequence of chromosome 3 of Plasmodium falciparum
0 1 147.4 3 144.4 3 144.4 4 3 144.4 6 0 0 0 1443.6 0 0 0 1423.6 0 0 1423.6	7 8 10			18 20 20	23 23 4				36 12 37 12 38		c 43 126.4 c 44 126.2 45 126.2		RESULT 1 PFMAL3P5/c LOCUS DEFINITION P1 ACCESSION AL		SOURCE ma	REFERENCE 1 AUTHORS BC CP	MC Residence of the second sec
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM nucleic - nucleic search, using sw model	Run on: August 21, 2002, 01:57:11; Search time 5413.87 Seconds (without alignments) 9562.892 Million cell updates/sec	Title: US-09-763-957-3 Perfect score: 2474 Sequence: 1 ttacagatacacagaatcagtaaccacatacaccatatgg 2474	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 1797656 seqs, 10463268293 residues	eq length: 0	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	<pre>GenEmbl:* : gb_ba:* : gb_htg:*</pre>	3: gb_in:* 4: gb_om:* 5: gb_ov:*	0: go_pat:* 7: gb_ph:* 8: gb_pl:*				21: em_or:* 22: em_ov:* 23: em_pat:* 24: em_ph:* 25: em_pl:*		29: em_v1:* 30: em_htg_hum:* 31: em_htg_inv:* 32: em_htg_other:*	를 다 다 다 다	Result Query No. Score Match Length DB ID Description

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(bases 1 to 86827)

Lawson, D., Bowman, S. and Barrell, B.

Direct Submission

Submitted (17-DEC-1998) P.falciparum Genome Sequencing Consortium,

The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
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On May 14, 2001 this sequence version replaced g1:2982535
On May 14, 2001 this sequence version replaced g1:2982535
g1:2982554 g1:2894454 g1:2982554 g1:2982554 g1:2894489 g1:2982572
g1:2922574 g1:4439391.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.
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PFC0575w (revised)"
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816. .825
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(revised of PFC0575w)"
                                                                                                                                                   Bowman, S., Skelton, J., Churcher, C., Lawson, D., Quail, M. and
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99376085
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AUTHORS
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JOURNAL
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'note="potential splice acceptor sequence for
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/gene="PFC0581w"
/note="potential splice donor sequence for
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/gene="PFC0581w"
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/gene="PFC0581w"
/note="potential splice donor sequence
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/gene="PFC0581w"
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9361. .9368
/gene="PFC0581w"
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/gene="PFC0581w"
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/gene="PFC0581w"
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/gene="PFC0581w"
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llarity 45.7%;
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NVITTQTYRENENENSDKISALVEYRNVSLSSIINSSQDDEGKKKYGIKFENYYVSYK
KKIPLVNGTYKYIDEPEKLNINMYALKNOKTGIVGKSGAGKSTILLESILGLINISOG
KTYVEGERDIRTYKYEGEDSIIGILAQSSEYNWINTENEYNNFTDDELYHALKIN
GINLGKNDLYKWHKQDMKSNYKKIIQTSKVINQSNDWTILLNDETRYLSLYRALKIN
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TKIWKETIKKKRQNYEKETDRWNHNREDEWHYKRANIYLYKVHKLINITLKDLTNPI
HDKEETITTWIKWIQEDIEYFLFNLQVEWLRILTLELFYKNKE"
COMPIEMENT(32477. .32486)
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                                                                                                                                                                               /gene="MAL1P3.03"
/note="MAL1P3.03, putative ABC transporter, len: 1822 aa"
/note="possible cenl, region of very high [A+T] content"
14884. .20352
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complement(32669. .32674)
/gene-"MALIP3.04"
/note-"potential splice donor sequence, aaa/gtatat"
join(36657. .36743,36864. .37343)
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/gene="MALIP3.04"
/gene="MALIP3.04"
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23896. .31533
/gene="FRNA"
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                                                                             /gene="MAL1P3.03"
14884. 20357
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Submitted (24-522.)

The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge (210.)

The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge (210.)

On Dec 16, 1999 this sequence version replaced gi:5763807.

For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="MALIP3.01"

complement(join(1748. .2598,2748. .2848,2990. .3276))
/gene="MALIP3.01"
/note="MALIP3.01, conserved hypothetical protein, len: 412
aa, similarity: UPF0006 family eg to
YBL055C/YBL0512/YBL0511, YBF5_YFBAST (418 aa), fasta
scores: opt: 316, E(): 1.1e-12, (33.2% identity in 271 aa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation-"MKLVFHYIKYINVLFYISIIFLKSNSLKIYNDLRYISTVNKYKV
LQIKKRSNLKKNHNIRKMEDNESSFIDIGSNLTDKMFDGVYNSKKHENDLQNVLNRAK
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NINKYPKIIITCTCLAEIDKSLKICETYDPEGKFLYLSAGVHPTNCYFFIDKKHEEKE
NEKKEYEFIKYFKNEVONSKMENDKKICDGEKDMNNLNEILLEKNLDTIPGFKY
NEKDKEYLENLKNKIIKYPNRIVCIGEIGLDFDRLYFCSKYIQIKYFIFOLKLYOMFN
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CSLKSLENINAVKKIPLNLLLLETDAPWGGVKKTHASYEXIKDTYEKRATTKK
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Amrklisgeinsiklingdelkiklndekhkdstkwdksysfisnleekysgtdlfr
Kkgeineantkiiedroefyilnndeieniatrfvlennfdelyigsfkgslidiigs
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/protein_id="CAB63556.1"
/db_xref="GI:6594244"
                                                                                                                                                                  Bowman, S., Churcher, C., Harris, B., Harris, D., Lawson, D., Quail, M. and Barrell, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Plasmodium falciparum"
/strain="3D7"
/db_xref="taxon:5833"
/chromosome="1"
complement(join(1748. .2598,2748. .2848,2990. .3276))
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/gene="MALIP3.01"
/note="potential splice acceptor sequence"
complement(2742 ...2747)
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/note="potential splice donor sequence, atg/gttaaa"
/gene="MALIP3.01"
/gene="MALIP3.01"
/gene="MALIP3.01"
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/gene-"MaliP3.02" 5005. 5496
                                                                                             Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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/db_xref="GI:6594245"
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        malaria parasite P. falciparum.
Plasmodium falciparum
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/gene="MAL1P3.02"
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                                                                                                                                  (bases 1 to 67970)
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DKKKEENSEVWSLYKTGQHKPKNATEHGEENLYEENVSEINNNAGGGLLLSSPYQYRE
GGGGGIISSYHETSNDTKDNDKENISEDKKEDHOOEEMLKTJLDKERKOKBKEKENE
KIEKKKKOEEKEKKQEKERKOEKERKOCKERROKOEKENKOKKIESEKKKKE
HDKRNEETWOQPOOTSEETNNEINVPLPSPLTDVTTPEEHKEGEHKEEEHKEGEHKEE
EHKEEEEHKEEEHKKEEHKSKEKKKKKKOVIEDE
                                                                                                                                                         /translation="WritkMNSGIFFIKLLICISFICVFECFNKCMISYRKDLIWYSEN
CFNYSIDRSLAEGSSESKETKVKDIPNIELLKSLNINYEEYEKMKEIVGSFMDNNNLN
IANEVLKNIHSFINIENIFSLINDSSKSPVLKTFLKEFGSIFPHMLNNVPKLLFDLCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"hypothetical garp protein"
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/translation-"MNVLFLSYNICILFFVVCTLNFSTKCFSNGLLKNONILNKSFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ITGRLINETELEKNKDDNSKSETLLKEEKDEKDDVPTTSNDNLKNAHNNNELSSSTDP
TNI INVNDKDNENSVDKKKDKKEKKHKKDKKEKKEKKDKKEKKDKKEKKHKKEKKHKK
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36854. 36863
/gene="MALLP3.05"
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hoote="potential splice donor sequence, aag/gtaaca"
join(45d11 .46396,46562. .50233)
/gene="MALIP3.07"
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                                                                                                                                                                                                                                                                                                                                                                                                               .40284))
                         join(365), .35/43,30504. .37,343,
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                                                                                           /product-"hypothetical protein, MALIP3.05"
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complement(join(38049. .39995,40210.
                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="garp"
/note="Mill3.06, garp, len: 673 aa,
ldentical to GARP_PLAFF (678 aa), fas
identity in 678 aa overlap"
                     .36743,36864. .37343)
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                                                                                                                                                                                                                           RNPLHIILGLIVILAAIYVFENFKNFEC'
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/gene="MAL1P3.05"
/gene="MAL1P3.05
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                                                                                                                    attaatgaagcattgtagtataaaggagtctagaataaatttcttaaatattagaggaa-a 1222
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                                                        TTAAAATTATAAATTAAATATAATTAAATTAAATTATATTAAATGAATTAAATGAAATA
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                                                                                                                                                                                                                                                                                                                                                                                         Submitted (05-FEB-2002) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louls, MO 63108, USA USA Control of Medicine version replaced q1:15625013.
                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 172816)
Waterston, R. H.
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Homo sapiens chromosome 2 clone RP11-724016, complete sequence. AC093899 AC068884 AC093899.3 GI:18497265
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Feb 5, 2002 this sequence version replaced gi:15625013.
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Web site: http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@watson.wustl.edu
Center project name: H_NH0724016
Drafting center: WIBR
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-724016"
53405 a 33788 c 33104 g 52519
                                                                                                                                                                                                             The sequence of Homo sapiens clone Unpublished
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Waterston, R.H.
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                                                                                             Mitochondrion Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Petrygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Epiydroidea; Drosophilidae; Drosophila.

[ (bases 1 to 4601)
Lewis, D.L., Farr, C.L., Farquhar, A.L. and Kaguni, L.S.
Sequence, Organization and Evolution of the A+T Region of
Mol. Biol. Evol. 11, 523-538 (1994)
                         DMU11584 4601 bp DNA linear INV 23
Drosophila melanogaster Oregon-R mitochondrial A+T region.
U11584
                                                                                                                                                                                                                                                        Submitted (28-JUN-1994) Laurie S. Raguni Ph.D, Dept. of Biochemistry, Michigan State University, East Lansing, MI, 48824-1318, USA
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                                                                         mitochondrial DNA; A+T region; tandem repeats fruit fly.
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/organelle="nitochondrion"
/strain="Oregon-R"
/db_xref="taxon:7227"
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45.7%; Pred. No. 4.8e-10;
tive 0; Mismatches 774;
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/note="repeat II-B1"
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IMMMSTLITLFFYLRICYSAFWMYFENNWIMKMNMNSINYNWYMIMTFFSIFGLFLI
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                                                                                    7 (bases 14215 to 14512)
Ballard,J.W., Olsen,G.J., Faith,D.P., Odgers,W.A., Rowell,D.M. and
Atkinson,P.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Department,
USA
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sequences; sequence is a composite containing sequences
obtained from different Drosophila melanogaster strains"
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join(1470. .1472,1474. .3009)
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Evolution of Drosophila mitochondrial DNA and the history of melanogaster subgroup
                                                                                                                                                                                                                                                                                                                                                           p (bases 1 to 408; 13319 to 19517)
Lewis,D.L., Farr,C.L. and Kaguni,L.S.
Drosophila melanogaster mitcochondrial DNA: completion of the nucleotide sequence and evolutionary comparisons
Insect Mol. Biol. 4 (4), 263-278 (1995)
                                                                                                                                                 Evidence from 12S ribosomal RNA sequences that onychophorans
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                                                                                                                                                                                                                                                   Lewis D.L., Farr C.L., Farquhar, A.L. and Kaguni, L.S. Sequence, organization, and evolution of the A+T region brosophila melanogaster mitochondrial DNA MOI. Biol. Evol. 11 (3), 523-538 (1994)
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Lewis, D.L., Farr, C.L. and Kaguni, L.S.
Direct Submission
Submitted (03-027-1995) Laurie S. Kaguni, Blochemistry D
Michigan State University, East Lansing, MI 48824-1319,
Location/Qualifiers
1.19517
/organelle-"mitochondrion"
                                Proc. Natl. Acad. Scl. U.S.A. 87 (24), 9558-9562 (1990)
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Science 258 (5086), 1345-1348 (1992)
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171. .230
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de Bruijn, M.H.
Drosophila melanogaster mitochondrial DNA, a novel organization and
genetic code
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Transfer RNA genes in Drosophila mitochondrial DNA: related 5'
flanking sequences and comparisons to mammalian mitochondrial tRNA
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    2189 AGTTTTAATTATAATAAATTTATGAATAGGGGGAATAAATTTATTTTCATTTTACATA 2130
                                                                 attatttataaatccattagagatttaagttaatgtctctctttgattttaacatggttc 1864
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Mitochondrion Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (Bases 12511 to 12682)
Glary,D.O., Goddard,J.M., Martin,S.C., Fauron,C.M. and
Wolstenholme,D.R.
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Analysis of nucleotide substitutions of mitochondrial
Drosophila melanogaster and its sibling species
MOI. Biol. Evol. 4 (6), 638-650 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila mitochondrial DNA: a novel gene order
Nucleic Acids Res. 10 (21), 6619-6637 (1982)
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Genetics 118 (4), 649-663 (1988)
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Satta, Y. and Takahata, N
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HSWTVPALGVKVDGTPGRLNQTNFFINRPGLFYGQCSEICGANHSFMPIVIESVPVNY
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LSLALPLMLCFMLYGWINHTQHMFAHLVPQGTPAILMPFMVCIETISNIIRPGTLAVR
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FRESLSPAIELGASWPPWIISRNPPOIDFLLWATLLASGYTWAHHSLMENNHSQT
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/db_xref="GI:1166532"
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/db_xref="G1:1166534"
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/note="TAA stop codon
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3840. .3906
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/transl_table=5
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                                                                                                                                                                      /product="tRNA-Leu"
3083. .3767
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/product="tRNA-Gly"
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3907. .4068
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6119. .6183
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                                         complement(6337..6401)
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complement(6401.8124)
/note="TAA stop codon is corresidue to the mRNA"
                                                                                                                                  Score 143.6;
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                                /product-"tRNA-Glu"
                                                                                                                                  5.8%;
                     6252. .6318
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Submitted (25-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
3 (bases 1 to 159618)
Waterston, R. H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
11 (bass 1 to 159618)
Waterston, R.H.
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                                         aatattcaaagtaaataatagatataattcatcattcaatacgagtaattcaatctatta 1624
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On Oct 25, 2001 this sequence version replaced gi:16259145.
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Center: Washington University Genome Sequencing Center
Center code: WUGSC
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                                         Ouery Match 5.8%; Score 142.6; DB 9; Best Local Similarity 46.8%; Pred. No. 2.3e-10; Matches 671; Conservative 0; Mismatches 739;
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                                                                                                                                                                           1. .159618
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/clone="RP11-426F15"
51014 a 29807 c 29529 g 49268
                                                                                                                                                           Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (25-OCT-2001) Genome (Moniversity School of Medicine, 400 65108, USA
On Nov 2, 2001 this sequence ve.
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AC098590.2 GI:16596634
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Center: Washington University Genome Sequencing Center

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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47.0%; Pred. No. 3.3e-10;
tive 0; Mismatches 746; Indels 16;
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1403: gap of unknown length
10587: contig of 9184 bp in length
10687: gap of unknown length
57426: contig of 46739 bp in length
57526: gap of unknown length
110116: contig of 52590 bp in length
110216: gap of unknown length
110216: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 8.44 in Q20 bases; agarose-fp
Quality coverage: 8.54 in Q20 bases; sum-of-contigs
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chemistry: Dye-primer ET: 0% of reads
Chemistry: Dye-primer ET: 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of re
Assembly program: Phrap; version 0.990319
Consensus quality: 171367 bases at least 040
Consensus quality: 172444 bases at least 040
Consensus quality: 172546 bases at least 020
Insert size: 172000; agarose fp
Insert size: 173080; sum-of-contigs
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/note-"assembly_name:Contig14"
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/note="assembly_name:Contig12"
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1404. .10587
/note="assembly_name:Contig11
                                                                                                                       ------ Summary Statistics

    .172724
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

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Sequencing vector: plasmid; 68%
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Homo sapiens chromosome 4 clone RP11-426F15, complete sequence. AC096750 AC086887 AC096750.3 GI:16418260
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Submitted (25-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
J (bases 1 to 159618)
Waterston, R. H.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 159618)
Waterston, R. H.
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Submitted (25-007-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
MO 63108, USA
On Oct 25, 2001 this sequence version replaced g1:16259145.
                                            ctttgattttaacatggttctaaaaattaggtttaatcattgcgtcctcaatgaacccat
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Waterston, R.H.
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                                                                                                                                                                                                                                                               --aagattggtgactattcaattaattagttgtgaattgatgacaaatatttcatgagca
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                                                                  tttcctcaagtttagccatttttatgaaattaaacttaatcactactattaggtaaatt
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On Dec 16, 1999 this sequence version replaced g1:5763807.
For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is n progress and the correct sequence may based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
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NEKDYEENLKNKIIKYPNRIVCIGEIGLDFDRLYFCSKYIQIKYFIFQLKLVQMFN
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    aagttaatgtctctctttgattttaacatggttctaaaaattaggtttaat-cattgcgt 1889
                                                                                                                                                                                                                                                                                                                                                                                                   octcaatgaacccatgctatatgttttaaagttttttgtttttgacaatgtttttatt 1949
                                                                                   malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 67970)
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Plasmodium falciparum MAL1P3, complete sequence.
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KEFKLIKKENMESRAFKYINIFRMKEMKYCKIRLYFENSTGYFISSISOLYVEVYLFFI
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KKEEF SHINNSSANSTWANBEREKKRNNEYITKLENCSFELSYDNYKCHONHLIKNINFN
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TLONFLIEDILDNYQYEVNITKYRGNISEVMEKNNINJTKESHWGYSKLNY
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YISFLKDFKVFSGLVVVWIMFFHLFFEALLHFYFHLFTINLKVSLMYFLYKINLCSNN
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TYLDYTYTRNSDKEELYKPLYKDTHEERNKSSSMPFVKSSRNINNDRSFRYENDNSSS
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TILOKOVRYLEYFVILDFISLVYSGICFSMIIYGNITSAIKVHNNILYSILNADLYIF
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IILIYFFVFKRFSRGCKEAQRLYLSCHTPLCNIYSNALSGKNIINIYKKNTYHLDVYE
HYINNFRISYFFKWLINIWASLYIKIFILLLTTYIIMHPHLYASGIIKLYKEKNYVRI
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GINLGKNDLYKYMHKQDMKSNYKKIIQTSKVINQSNDNTILLTNDCIRYLSLVRLYLN
RHKYKIILIDEIPIFNLNNSVHDELNSFLIGKAKSFNYIIRNHFPNNTVLIISHHANT
LPWFLHMRNCSETFFKIVDIYKFLFEKNGGVIHSFTDKEDIVHIIVQNYKNLYIGVNG
CSLKSLENINAVKKIPLNLLLLETDAPWCGVRKTHASYEYIKDTYEKRAYTNLKKIKN
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DYIINFIKSTKKMEKDSLNENRSLPNVNIYNIMFSDVPSVTFFVTSCINLFNVFVKIF
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KKIPLVNGTYKYIDEEPSLKNINMYALKNQKIGIVGKSGAGKSTILLSILGLINISQG
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5005, 5496
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23896. .31533
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gene

CDS

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/translation-"MKKSYTFINVTILLFLTYLLLFLTYYNYDTFSKTKFNNNIKIDIN
RFKRIJAEASEEQKYPWEEDECLILNEEELIRPEHNDSPYLPEHYENIDKINELSINS
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HDKEETITTWIKWIQDELEYFLFNLQVEWLRILTLELFYKNKE"
complement (32477. .32486)
                                                                                                                                                                                                                                  Complement(join(31966. .32476,32675. .32775))
/gene="MALIP3.04"
/note="MALIP3.04, conserved hypothetical membrane protein, len: 203 aa, similarity: P. falciparum chromosome 2, PFB0110W, 096126 predicted integral membrane protein (255 aa), fasta scores: opt: 335, E(): 4.9e-15, (36.1% identity in 191 aa overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation-"mrikmusgiffikilicisficvfecfnkcmisyrkdilmysen
Cfnysidrslaegssesketkvkdipniellkslninyeeyekmkeivgsfmdnnnln
Ianevlknihsftnienifslindsskspvlktflkefgsifphmlnnvpkllfblcq
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/prodein_id="CaB63561.1"
/db_xref="G1:6594249"
/translation-"MNVLFLSYNICILFFVVCTLNFSTRCFSNGLLKNONILNKSFDS
ITGRILNETELEKNEDDNSKSETLKREKDEKDDYPTTSNDMIKNAHNNNEISSSTDP
ININNVNDKDNENSYDKKDKKEKKHKKDKKEKKEKKDKKEKKEKKDKKEKKHKK
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QGGCJISSYHTSNDTKDNDKENISEDKEDHQDEEMLKTLDKKERKQKEKEMKEDE
LEKKKKQEEKEKKQEKERKKQEKERKQOKEREMKQKEKEMKKKEH
HDKENEETMQQPDQTSEETNEMTEMPLASPLTDVTTPEEHKEGEHKEEEHKEGEHKE
EHKEEETMQPLOSTSETNURIMPLASPLTDVTTPEEHKEGEHKEEEHKEGEHKE
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identical to GARP_PLAFF (678 aa), fasta scores: 97.6%
identity in 678 aa overlap"
"region containing small subunit, 5.8S and large t rRNA genes and spacer regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="potential splice donor sequence, aaa/gtatat"
join(36657...36743,36864...37343)
/gene="MALIP3.05"
join(657...36743,36864...37343)
/gene="MALIP3.05"
/note="MALIP3.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNPLHIILGLIVILAAIYVEENFKNFEC"
36744. .36749
/gene="MALIP3.05"
7note="potential splice donor sequence, aag/gtatga"
36854. .38863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="conserved hypothetical membrane protein,
MALIP3.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="MALLP3.05"
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                                                                                                                                                                              complement(join(31966. .32476,32675. .32775))
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/gene="garp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-"hypothetical protein, MAL1P3.05"
/protein_id-"CAB63560.1"
/db_xref-"GI:6594248"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"potential splice acceptor sequence"
complement(32669. .32674)
/gene-"MALIP3.04"
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/db_xref="GI:6594247"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8907
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                                                                                                                         611 ttttggtaagtacaacttttctactcttatttaatggagggattatttttccatatacc 670
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                                                                                                                                                                                                                                                               aaacttaatcactactattaggtaaattcatatgtatcattaac----aatttcaatg 844
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                                                                                                      Gaps
                      /gene="garp"
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joln(45401. .46336,46562. .50233)
/gene="MALIP3.07"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tattcataaaaaaaatacacttaa---ataagtaacaataataaaaaacattatataaaga
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                                                                             Length 67970;
                                                                                                    24;
/note="potential splice acceptor sequence" complement(40204. .40209)
                                                                                         Pred. No. 1.1e-09;
0; Mismatches 648; Indels
                                                                              Score 138.2; DB 3;
                                                                             5.6%;
                                                                                                   Matches 621; Conservative
                                                                                          Similarity
          misc_feature
                                                                              Query Match
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168698 bp DNA linear PRI 09-JAN-2002
Homo sapiens BAC clone RP11-813K12 from 2, complete sequence.
AC068138
AC068138.6 GI:15638958
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The sequence of Homo sapiens BAC clone RP11-813K12
Upublished (2001)
S Waterston, R. H.
S Waterston, R. H.
Direct Submission
University School of Medicine, 4444 Forest Park Parkway, St. Lou Mo 6310B, USA
A (bases 1 to 168698)
E 4 (bases 1 to 168698)
S Waterston, R. H.
Direct Submission
University School of Medicine, 4444 Forest Park Parkway, St. Lou Mo 6310B, USA
L (bases 1 to 168698)
S Waterston, R. H.
Direct Submission
L Direct Submission
University School of Medicine, 4444 Forest Park Parkway, St. Lou University School of Medicine, 4444 Forest Park Parkway, St. Lou University School of Medicine, 4444 Forest Park Parkway, St. Lou Submitted (18-SEP-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Lou School R. S Waterston, R. S Wa
                                                                                                                                                                                                                                                                                                                             aagaattatcttatctcccgtatatttgtagatgttaaatgtaacgggcttagactgatg 1792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-JAN-2002) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63 On Sep 18, 2001 this sequence version replaced gi:15148349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelé
Eukamalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 168698)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Web site: http://genome.wustl.edu/gsc
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AUTHORS
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NOTICE: This sequence may not represent the entire insert of this cone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
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This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MCPherson, Department of Genetics, Washington University, St. Louis
MCP. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The Reci-11 human BAC library was made from the blood of one male donor, as described by Osoegawa.K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J. J. and de Jong, P. J. (1998). An Improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:18. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or pleter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)

The clone sequenced to the left is RP11-314B1, 2000 bp overlap; the clone sequenced to the right is RP11-86017. Actual start of this clone is at base position 161288 of RP11-314B1; actual end is at base position 166698 of RP11-813X12. NEIGHBORING SEQUENCE INFORMATION:

Data from AC069383 was used to finish this clone, AC068138.An unresolved di-trinucleotide repeat exists between 52436 and 52756

FEATURES

Location/Qualifiers
1. 168698
Acryanisms"Homo sapiens"
Ab_xref="taxon:9606"
/chromosome="2" 747. .778 /rpt_family="AT_rich" 984. .1004 /rpt_family="AT_rich" 'clone-"RP11-813K12" clone_11b="RPCI-11" /map="2" repeat_region repeat_region repeat_region

rpt_family="GA-rich" 078. .2122 rpt_family-"MIR" 689. .1746 rpt_family-"L1" 'rpt_family-"L2" repeat_region repeat_region repeat_region

rpt_family~"MER1_type" rpt_family="(TAAAA)n" 5137, 3594 /rpt_family="ERVL" 5819, 5022 /rpt_family-"L1" 1780. .2806 repeat_region repeat_region repeat_region repeat_region repeat_region

6798. .6956 /rpt_family="L1" 6836. .6854 /rpt_family="L1" 6855. .6939 /rpt_family="L1" 6940. .7021 repeat_region repeat_region

repeat_region

rpt_family="L2" 6186. .16419 'note="match to EST BI915240 (NID:g16179345)" /rpt_family="(GGAA)n" 13377. 1360-/rpt_family="(CAAA)n" 15177, .15954 14013, .14059 /rpt_family="A-rich" 14327, .14400 /rpt_family="MaLR" 14503. 1460-/rpt_family="MaLR" 4969. .14988 /133. .7366 /rpt_family="L1" 7818. .70^ .y-"Alu" /rpt_family="L1" 7080. .7132 /rpt_family="L1" y-"MIR" 818. .7904 rpt_family="L1" 1908. .8117 /rpt_family-"Ll" 14988 .16086 .17681 /rpt_family /rpt_family 15905. .160 7644. repeat_region misc_feature

'rpt_family-"AT_rich" 7930 rpt_family="AT_rich" 7957. 1826 'rpt_family="AT_rich" 7683. .17812 /rpt_family="(A)n" 21362, .210ce rpt_family-"MalR" /rpt_family="11" rpt_family="Alu" 0428. .20450 /rpt_family="L1" 8289. 18571 y="L1" /rpt_family="L1" 8669. 1075 /rpt_family="L17836" repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region

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2977. .23195
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Location/Qualifiers
1. 349980
[Organism="synthetic construct" | A19980
[Abore="chemically treated genomic DNA (Homo sapiens)-Original length of seq 1: 3 673778 <2233-split as sapiens)-Original length of seq 1: 3 673778 <2233-split as follows.-seq 01 0.000.001 TO 0.349.980-seq 02 0.300.001 1.349.980-seq 03 500.001 1.549.980-seq 04 900.001 1.349.980-seq 06 1.500.001 1.849.980-seq 08 1.000.001 2.449.980-seq 09 2.400.001 2.749.980-seq 10 2.700.001
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                                              tattataatcatatattagataaatatacaaatatttgttaaattttacattattattt
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                              ataatttaataagtattgaatgtagaataatttttatttataaatttgaactaaaatatt
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Olek,A., Plepenbrock,C. and Berlin,K.
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Sequence 6 from Patent W00200932.
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                                                                                                                                                              Length 168698;
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33036. 33221
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3335. 33354
/rpt_family="(CA)n"
3743. 33597
/rpt_family="(CA)n"
/rpt_family="(CA)n"
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Plasmodium falciparum

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

L (bases 1 to 14867)

Gardner, M.J., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, L.,

Koonin, E.V., Shallom, S., Mason, T., Yu, K., Fulji, C., Pederson, J.,

Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M.,

Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O.,

Salth, H.O., Fraser, C.M., Hoffman, S.L. et al.

Chromosome 2 sequence of the human malaria parasite Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (02-NOV-1998) The Institute for Genomic Research, 9712
Medical Center Drive, Rockville, MD 20814, USA
Location/Qualifiers
atacacttaaataagtaacaataataaaaaacattatataagagattaagataatttaat 1509
                                                                                                                                                tcaaagtaaataatagtataattcatcattcaatacgagtaattcaatctattataatc
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2 (bases 1 to 14867)
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/organism="Plasmodium
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/gene="pFB0495w"
11241. 14606
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/note="preddicted by GlimmerM"
/codon_start=1
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Plasmodium falciparum chromosome 12, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.
AC005504.3 GI:4558584
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                                             Eukaryota: Alvoolata: Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 104992)
Hyman, R.W., Fung, E.L., Qin, F., Tamaki, T., Kurdi, O.B., Conway, A.B. and Davis, R.W.
Plasmodium falciparum 3D7 chromosome 12
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Hyman, R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
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58842: gap of unknown length
91011: contig of 32169 bp in length
91211: gap of unknown length
104992: contig of 13781 bp in length.
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AC004157 169546 bp DNA linear HTG 12-AUG-2000 Plasmodium falciparum chromosome 12 clone 3D7, *** SEQUENCING IN PROGRESS ***, 2 unordered pieces.
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malaria parasite P. falciparum.
Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                               Submitted (19-FEB-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto,
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                     Mao, J., Tamaki, T.,
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NOTE: This is a "working draft' sequence. It currently

consists of 2 contigs. The true order of the pieces

is not known and thair order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.
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23666: gap of unknown length
169546: contig of 145880 bp in length.
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Pred. No. 1.4e-09;
0; Mismatches 664; Indels
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                      Rowley, D.,
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/db_xref="taxon:5833"
1 (bases 1 to 169546)
Hyman, R.W., Fung, E.L., (in, F., Rowley,
Kurdi, O.B., Conway, A.B. and Davis, R.W.
Plassmodium falciparum 3D7 chromosome 1
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/clone="PFYAC293"
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Best Local Similarity 47.8%;
Matches 633; Conservative
                                                                                                               Hyman, R.W., Oln, F. Direct Submission
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tottaaatattagaggaaaactattttaaaaaattacaagaaaagtttgatotataaco 1263
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                                                            Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA
On Apr 2, 1999 this sequence version replaced 91:4337172.
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                                                                                                                Apr 2, 1999 this sequence version replaced 91:4337172.
NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pleces is not known and their order in this sequence record is
 Unpublished
2 (bases 1 to 104992)
Hyman, R.W. Olin, F., Fung, E.L., Conway, A.B. and Davis, R.W. Direct Submission
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DNA encoding 1-ami

Genomic clone LE-A Crucifer 1-aminocy 1-aminocyclopropan Broccoli ACC synth Zucchini ACC synth

score:

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Sequence:

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Run on:

Scoring table:

Total number Minimum DB Maximum DB

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Searched:

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Mung bean; 1-aminocyclopropane-1-carboxylic acid synthase;
ACC synthase; AIM-1; promoter; pGEL-1; transgenic plant; ss.
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AAV30324
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AAQ15139
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AAV15701
AAD04541
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AAY79292

Isolated nucleic acid molecule for producing transgenic plants have altered characteristics such as resistance to a plant pathogen comprises promoter, inducible in response to physical stimulation

English 111pp; Page 98-101; Claim

1-aminocyclopropane-1-carboxylic acid synthase (ACC synthase, see AAY79292). The ACC synthase gence, AIM-1, is induced in response to mechanical strain, auxin and salt stress. The invention relates to the pGEL-1 promoter (see AA294266) that directs expression of the AIM-1. gene. pGEL-1 is capable of induction by physical and/or environmental stimuli in cells in which it is indigenous and, in the absence of any negative regulatory mechanism, is capable of constitutive expression in cells in which it is non-indigenous. The promoter can be used to direct expression of genes conferring useful traits on plants, such as improved resistance to a plant pathogen, altered autilitional characteristics, expression of a plantabody, altered biochemical pathway, altered expression of extreme to a plant pathogen. The colour. bean mung sequence is that of cDNA encoding present The

T; 0 other; G; 566 C; 426 BP; 548 A; 383 Seguence 1923

ö 180 120 180 240 300 300 360 420 420 480 480 9 Gaps 9 9 actecacactetaaccacatacaccatatgggttteaaggeeatggaccaaactecettg aaggottatgatcaaaaccocttcatccacagataatcctaacggtgttatgcaaatg gattatcatggtctggccgagttcagaaatgctgtggctaaatttatggctagaacaagg tattatccaggctttgaccgggatttgaggtggagacaggagttaaacttgttccagtt Length 1923; ö Indels 21; ö DB 100.0%; Score 1923; 100.0%; Pred. No. 0; iive 0; Mismatches Conservative Similarity Query Match Best Local Simi Matches 1923; П Н 241 301 61 121 121 241 301 361 361 421 541 61 181 421 481 481 541 601 601 g å g Q à g õ 셤 ò g g g ò ò ç ò à g q ò å

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                                                                                                                                                                                                                                                                                       Poplar 1-aminocyclopropane-1-carboxylic acid synthase gene PNACCS1.
                                           Dzone; induction; exposure; resistance; transgenic plant; ACC1;
1-aminocyclopropane-1-carboxylic acid biosynthesis; ds.
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                                                                                                                                                                                                                                                                26-AUG-1997
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toggcatcatatactcttacaatgatgctgtggttaattgtgcacgcaaaatgtcaagct
                                  ttggattggtgtcaacacagactcagtatcttttagcatcgatgctaaatgatgatgagt
                                                                   ctggggggttggccaaagttggcataaagtgcttgca---aagcaatgctggtctatttg
                                                                                                                                                                  tgtggatggatttaaggcaacttctcaaaaagccaactttcgactctgaaacggagcttt
                                                                                              ttgtggagaggtttctggcagagagtgcaaagaggttggctcaaaggttcagggttttca
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Gaps

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Length 1864

41.1%; Score 791.2; DB 18; Length 73.0%; Pred. No. 4.5e-218; tive 0; Mismatches 378; Indels

Best_Local Similarity 73.0 Matches 1047; Conservative

110

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Query Match

aaactcccttgttgtccaagatggctattggggatggacatggcgaatcatcccatact 169

1163 1129 1186

1043 1009 1103

890 gcaacctcgtacacattgtttatagtctttcaaaggacatggggttccctggcttcagag

aacccggtttcataagcatagctgagatattagaggatgaaacagacatagagtgtgacc

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1366
                                                        ctttgcmacgmatccgcmactttgtgcttcmammcmaggaggtcgtggtgtctmataaga 1426
                                                                                    aacattgttggcacagtaacttgaggctgagcctcaaaaccagaaggtttgatgatatca 1486
                                                                      cttgtcaagaattaaaacatttgtcaataaagaggcggacaccaagaagtctaggaaga 1523
                                                                                                  acttgogctggcaaggcagtcttaaactgctcaactctcctcgaatatacgatgatttca 1583
                                                                                                                                                                                                                         Papaya; ACC synthase; ethylene biosynthesis; fruit ripening; enzyme;
1-aminocyclopropane-1-carboxylic acid synthase; regulation; ds.
                          Papaya ACC synthase cDNA sequence - useful for regulating ethylene
biosynthesis in the ripening of fruit
                                                                                                                                                                                                                                                               Location/Qualifiers
17..1480
/*tag= a
/Product= "Papaya ACC syntase"
                                                                                                                                                                                                           Papaya ACC synthase encoding cDNA.
                                                                                                                                                                 AAV31482 standard; cDNA; 1888
                                                                                                                                                                                                                                                                                                                              95US-0485107
                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                            95US-0485107
                                                                                                                                                                                                                                                                                                                                                                        Stiles JI;
                                                                                                                                                                                                                                                                                                                                                        (UYHA-) UNIV HAWAII.
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                                                                                                                                                                                                                                          . Carica papaya.
                                                                                                                                                                                              13-AUG-1998
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                                                                                                                                                                                                                                                                                                                                                                       Neupane KR,
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This cDNA encodes a papaya 1-aminocyclopropane-1-carboxylic acid synthase production and control of ACC synthase in transformed plants and cells, especially to control of ACC synthase in transformed plants and cells, sepecially to control fruit ripening. The enzyme converts and cells, responsible for the ripening of fruit (ACC is converted to ethylene, which is responsible for the ripening of fruit (ACC is converted to ethylene by ACC oxidase). Commercial tropical fruit markets e.g. papaya production, require fruits in an adequately ripened state. Ripening is dependant on synthase coding sequences, the endogenous enzyme can be inhibited using antisense constructs, until it reaches its destination, then allowed to

Claim 1; Fig 1; 33pp; English.

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ripen, or be used in recombinant cells which can produce ethylene and turn ripen fruit. Control or inhibition of ethylene production with nucleic acids is safer than chemical means, which can be toxic, and cannot be used for commercial inhibition.
                                                                                                   Gaps
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                                                                                         119 tgttgtccaagatggctattggggatggacatggcgaatcatccccatacttgatggat
                                                                                                                        ggaaggettatgatcaaaaccetttcateceacagataatectaacggtgttatgcaaa
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                                                                  Length 1888;
                                                                                 Indels
                                     Sequence 1888 BP; 577 A; 354 C; 399 G; 558 T; 0 other;
                                                               Score 735; DB 19;
Pred. No. 8.1e-202;
0; Mismatches 400;
                                                           Ouery Match 38.2%;
Best Local Similarity 70.8%;
Matches 1013; Conservative
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                                     1002 aatttattgtagagagcagaaagaggctggcaatgagacatagtttttcacacaaagac 1061
                                                                                                                                                                                                                                                                                                                                    Poplar 1-aminocyclopropane-1-carboxylic acid synthase gene PNACCS2
                                                                                                                                                                                                                      1362 aaactagtettagaeteagetteteetetegetatgaggatateatggagaeaceegggtt
                                                                                                               ggtttctggcagagagtgcaaagaggttggctcaaaggttcagggttttcactggggggt
                                                                                 taaggcaacttctcaaaaagccaactttcgactctgaaacggagctttggaaagttatca
                                                                                           ---aaaaccagaaggtttgatgata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic enzyme genes - from poplar tree, are useful for generating ozone-resistant trees and pollution clean-up trees
                                                                                                                                                                                                                                                                                                                                                    Ozone; induction; exposure; resistance; transgenic plant; ACC;
1-aminocyclopropane-1-carboxyl1c acid blosynthesis; ds.
                                                                                                                                                                                                                                            1484 tcaccatgtcacctcactcccctacctcagtcacctatggttaaagcca 1534
BP
                                                                                                                                                                                                                                                                                        AAT73502 standard; cDNA to mRNA; 1868
                                                                                                                                                                                                        acagtaacttgaggctgagcctc-----
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119..1579
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/product= PNACCS2
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                                                                                                                                                                                                                                                                                                                      (first entry)
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This sequence, designated PNACCS2, is a 1-aminocyclopropane-1-carboxylic acid (ACC) synthase gene isolated from poplar trees which had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone for 6 hours after one hour acclimation at 25 degrees C, 70 % relative humidity, 30 k lux and air current 30 cm/second. This gene will be
                                                                                                                                                                                                                                                                                                                                                                            358
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                                                                        humidity, 30 k lux and air current 30 cm/second. This gene will be useful for breeding air pollutant ozone-resistant trees, especially
                                                                                                                                                                                                                                                                                                                      tgttgtccaagatggctattggggatggacatggcgaatcatccccatactttgatggat
                                                                                                                                                                                                                                            138 ttttgtccaagattgcaacgaatgatagacatggagagaactccccatatttgatggat
                                                                                                                                                                                                                                                                      agogtatccaccttgtatgtgatgaaatatatgctgcaacagttttcagccaacccggtt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ctgaagcctccatttgcactccagaaggaataaatgatttcagggccatagctaactttc
                                                                                                                                                                                                                                                                                                                                                                                                                              aggattatcatggtctggccgagttcagaaatgctgtggctaaatttatggctagaacaa
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                                                                                                                              other;
                                                                                                                                                              Score 691.6; DB 18;
Pred. No. 2.8e-189;
); Mismatches 359;
                                                                                                                             C; 405 G; 507 T; 0
Pages 9-11; 12pp; Japanese.
                                                                                                                                                                                           -
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                                                                                                                                                                 36.0%;
71.7%;
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                                                                                                                                                                              Similarity
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Best Local :
                                                                                                    poplar
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                                          taaggcaactictcaaaaagccaactitcgacictgaaacggagcittggaaagitaica 1258
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/note- "antisense oligonucleotide (Claim 13)"
complement (51..100)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag* e
/note* "antisense oligonucleotide (Claim 13)"
complement (151..200)
                                                                                                                                                                                                                                                                                                                                                                        ACC synthase; 1-aminocyclopropane-1-carboxylate synthase; ethylene; transgenic plant; wilting; geranium; pPHSacc49; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag" d
/note= "antisense oligonucleotide (Claim 13)"
complement (101..150)
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/note= "antisense oligonucleotide (Claim 13)"
complement (251..300)
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/note- "antisense oligonucleotide (Claim 13)"
complement (301..350)
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                                                                                                                                                                                                                                                                                                                                                      Pelargonium 1-aminocyclopropane-1-carboxylase synthase cDNA.
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/note= "antisense oligonucleotide
complement (201..250)
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104..1576
                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (1.50)
                                                                                                                                                                                                                                                                                                    AAV30326 standard; cDNA; 1878
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1810..1815
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This cDNA clone, designated pPHSacc49 (ATCC 98179), codes for a construction of the control of geranium (Pelargonium x hortorum cv. Sincerity). (See AAW60235) of geranium (Pelargonium x hortorum cv. Sincerity). Construction of the 2-butoxyethanol precipitation technique. This was converted to cDNA and screened with a probe generated by PCR complification (see AAV30128-29). The PHSacc44 (see AAV30134) and pPHSacc44 (see AAV30134) and rose ACC synthase cDNA clone pARSacc44 (see AAV30134) and pPHSacc44 (see AAV30134) and rose ACC synthase cDNA clone pRoseKacc7 (see AAV3030), are also claimed. These ACC synthase gones, or their pPHSacc44 (see AAV30314) and antisense orientation under control contr
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/note= "any contiguous 50 nucleotides (Claim 13)"
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/note- "antisense oligonucleotide (Claim 13)"
complement (451..500)
         /note= "antisense oligonucleotide (Claim 13)"
complement (351.400)
                                                                                                                         /"cay" )
/note= "antisense oligonucleotide (Claim 13)"
complement (401..450)
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REAL PRESENTATION OF THE PROPERTY OF THE PROPE
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Juery match Best Local Similarity 70.8 Matches 1001; Conservative

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The present sequence encodes Coffea arabica, coffee-fruit specific 1-aminocyclopropane-1-carboxylic acid (ACC) synthase.

ACC synthase con be used to control ethylane blosynthesis in coffee plants, as ACC synthase is an element of the ethylane blosynthesis pathway. Transformation of wild-type coffee plants with constructs containing the CDNA can also be used to block ACC synthase synthesis. The CDNA can also be used to block ACC synthase synthesis. The CDNA can also be used to block ACC synthase synthesis. The cDNA can also be used to controlled action are incapable of synthesising ethylene, which is necessary in the final stages of fruit ripening in coffee, therefore ethylane application to the entire plant can synchronise controlled, e.g. application to the entire plant can synchronise ripening. Coffee beans are preferably obtained from mature fruit, but non-uniform ripening has necessitated laborious hand-picking, or low ytelds and productivity when harvesting by strip harvesting or mechanical techniques. The ability to synchronise ripening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e.g.
   gtggctctgaggaggatcataacatttgcacttcagaacaaggaagctgcggttttgcct
                                 -ctaataagaaacattgttggcacagtaactt---gaggctgagcctcaaaaccagaagg
                                                  ACC synthase and ACC oxidase from coffee, Coffea arablea - and encoding DNA, useful in methods to control coffee bean ripening e to allow synchronous ripening and thus more productive harvesting
                                                                                                                                                                                                                                                                                                                                           synthase;
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                                                                                                                                                                                                                                                                                                                                      Coffee-fruit; 1-aminocyclopropane-1-carboxylic acid s ACC synthase; ethylene biosynthesis; fruit ripening;
                                                                                                                1474 tttgatgatatcaccatgtcacctcactctcccc 1507
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/*tag= a
/product= ACC_synthase
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       Length 2088
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                     Indels
    ; DB 19;
.1e-184;
                   0; Mismatches
    672.8;
No. 8.1
    Score Pred. 1
   35.0%;
              912; Conservative
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Query Match
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                                                                                                                 This sequence represents the novel gene, miacc2, which is a member of the mango ACC synthase multigene family. ACC synthase an enzyme involved in the pathway for ethylene blosynthesis and the rate of endogenous expression of ACC synthase is considered to limit substantially the rate of ethylene production. Endogenous ethylene often deleterious to crops, especially if some form of mechanical
                                                                                                                                                                                                                                                                                                                     ACC synthase; S-adenosyl-L-methionine methylthioadenosine lyase; miacc2; ethylene biosynthesis; transgenic plant; senescence; antisense expression system; plant development; fruit ripening; EC 4.4.1.14; mango; multigene family; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                            /EC_number= 4.4.1.14
/Product= miacc2
/note= "Sequence represents 75% of the coding
sequence and does not contain the start
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pineapple, papaya and mango ACC synthase genes – used in gene
therapy to produce fruits with reduced senescence
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wounding has occurred and diminishes their post harvest quality and storage life. Novel ACC synthase genes expressed in transgenic plants using either sense or antisense expression system may be used to control the regulation of plant development, in particular fruit ripening, reducing senescence and thus improving storage life.
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                                                               G; 317 T; 0 other;
                                                                                             DB 18;
                                                                                                      Pred. No. 4.4e-173;
0; Mismatches 278;
                                                                                             Score 635.2;
                                                               Sequence 1113 BP; 320 A; 212 C; 264
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74.3%;
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(Note: Revised entry submitted to correct the patent number format of St Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpl/updates/ntis_us.html.)
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                                                    atggatttaaggcaacttctcaaaaagccaactttcgactctgaaacggagctttggaaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A lambda gt10 library was constructed using cDNA prepared from powdered, frozen fruit (i.e. tomatoes).

RNA isolated from powdered, frozen fruit (i.e. tomatoes).

Recombinant phage containing inserts were plated, transferred to an itrocellulose filter and hybridised to zucchini pACCI cDNA as probe (see AAQ15131). A full-length cDNA from tomato, designated pACCI was recovered. Additional clones were isolated using the see also AAQ15132-Q15140.
                                                                                                                                                                                                                                                                                                                                                                          1-aminocyclopropane-1-carboxylic acid synthase; fruit ripening;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding ACC synthase - used for control of plan for prodn. of ACC synthase, ethylene and ethanol
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                                                                                                                                                                                                                                                                                                                                              Clone ptACC1 encoding the tomato ACC synthase
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91..1548
/*tag= a
1732..1737
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                                                                                                                                                                                                                                                   AAQ15134 standard; DNA; 1775
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                                                                                                                                                                                                                                                                                                                     (first entry)
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              15;
 Length 1775;
              Indels
Score 630.2; DB 12;
Pred. No. 1.5e-171;
0; Mismatches 493;
32.8%;
            961; Conservative
      Similarity
      Best Local
Matches 96
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                                                                                                                                                                                                                                                                                                   Novel isolated DNA molecule encoding 1-aminocyclopropane-i-carboxylic acid synthase, LE-ACC2 useful for producing ACC synthase which is essential for the production of ethylene in higher plants
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             1251 agttattataaacgatgttaagcttaacgtctcgcctggatcttcgtttgaatgtcaaga
                                            tggggggttggccaaagttggcataaagtgcttgcaaagcaatgctggtctatttgtgtg
                                                         gccagggtggttagggtgtgctatgccaacatggatgatatggctgtgcaaattgcttt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tomato, 1-aminocyclopropane-1-carboxylic acid synthase, ethylene production; fruit ripening; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tomato 1-aminocyclopropane-1-carboxylic acid synthase,
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90US-0579896
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10-SEP-1990;
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                  tgtggagaggttctggcagagagtgcaaagaggttggctcaaaggttcagggtttcac
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 gecteaattegteagtatagetgaaateetegatgaacaggaaatgaettaetgeaacaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid synthase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             delayed fruit ripening; transgenic plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthase; conserved peptide;
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                                                                                                                                                Length 1818;
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                                                                                                                                                                     Indels
                                                                                                                  Sequence 1818 BP; 602 A; 282 C; 367 G; 567 T; 0 other;
                                                                                                                                                 DB 22;
                                                                                                                                                32.8%; Score 630.2; DB 22; 65.4%; Pred. No. 1.6e-171; ive 0; Mismatches 493;
         5; 92pp; English.
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Best Local Similarity 65.4
Matches 961; Conservative
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          Claim 1;
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us-09-763-957-1.rng

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The present sequence encodes tomato

1-aminocyclopropane-1-carboxylic acid (ACC) synthase. Tomato ACC

1-aminocyclopropane-1-carboxylic acid (ACC) synthase. Tomato ACC

1-aminocyclopropane-1-carboxylic acid (ACC) synthase. Tomato (LE-ACC) late (LE-ACC) late (LE-ACC) late (LE-ACC) and LE-ACC)

2-ACC LB) ACC synthases.

2-ACC LB) ACC synthases.

3-ACC synthases.

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3-ACC synthase (LE-ACC)

3-ACC synthases.

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3-ACC synthase (LE-ACC)

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3-ACC synthases.
                                                                                                                                                                                      A encoding anti-sense RNA blocking plant ACC synthase expression used for producing transgenic plants with delayed fruit ripening
                                                                                                                                                                                                                                 Example 3; Columns 63-68; 91pp; English
                  92US-0862493.
90US-0579896.
95US-0378313.
95US-0481171.
                                                                                      (USDA ) US SEC OF AGRIC
                                                                                                                    Theologis A;
                                                                                                                                              1998-206005/18
                                                                                                                                                              P-PSDB; AAW47313
                            10-SEP-1990;
25-JAN-1995;
07-JUN-1995;
                                                                                                                  Sato T,
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Sequence 2230 BP; 824 A; 314 C; 414 G; 678 T; 0 other;

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                                actititiacaciccacactctaaccacatacaccatatgggittcaaggccatggacca 110
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                                        aactecettgttgtecaagatggetattggggatggacatggegaateatececataett
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                       15;
     DB 19; Length 2230;
                     Indels
32.8%; Score 630.2; DB 19;
65.4%; Pred. No. 1.7e-171;
iive 0; Mismatches 493;
                   Conservative
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Query Match
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                                                                                                                                                                                                                                                                                                  Novel isolated DNA molecule encoding 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC2 useful for producing ACC synthase which is essential for the production of ethylene in higher plants
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Pred. No. 1.7e-171;
0; Mismatches 493; Indels 15;
                                    Tomato 1-aminocyclopropane-1-carboxylic acid synthase (ACC) DNA
                                                      1-aminocyclopropane-1-carboxylic acid synthase; production; fruit ripening; transgenic plant; c
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2230 BP; 824 A; 314 C; 414 G; 678 T; 0 other;
                                                                                                  Location/Qualifiers
91..1548
91..1547
Attag= a /Product= "Tomato ACC synthase"
                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                       deficient in ACC synthase.
                                                                                                                                                                                                                                                                                                                                      Claim 1; Column 67-70; 92pp;
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65.4%;
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                                                                                                                                                                                     95US-0378313
                  (first entry)
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                                                                                  Lycopersicon esculentum.
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                                                                                                                                                                                     25-JAN-1995;
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                  04-JUL-2001
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                                                                           caccggagcacacgaagtcactgcctttgtttggcagatcccggcgaggcattcttagt
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1-aminocyclopropane-1-carboxylic acid (ACC) synthase is essential for the production of ethylene in higher plants; ethylene is a determinant of fruit ripening. The present invention relates to an expression cassette which comprises the reverse transcript of RNA complementary to an RNA transcribed from ACC synthase gene. The expression cassette can be used to prevent ACC gene expression. The expression cassette is useful for inhibiting ethylene production and fruit ripening, when introduced into a plant or plant cells. The present sequence is the coding sequence for
                1478
                             Expression cassette for producing transgenic plants exhibiting inhibited ethylene production and delayed fruit ripening, comprises complementary RNA which inhibits 1-aminocyclopropane-1-carboxylic a
   taataagaaacattgttggcacagtaacttgaggctgagcctcaaaaccagaaggtttga
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                   gcaacgaatccgcaactttgt.......gcttcaaaacaaggaggtcgtgttc
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06-NOV-1995;
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               gccagggtggtttaggggtgtgtgtatgccaacatggatgatatggctgtgcaaattgcttt 1370
                                                                                                                                        1371 gcaacgaatccgcaactttgt-----gcttcaaaacaaggaggtcgtggtgtc 1418
cgtcgataattttctaagagaaagcgcgatgaggttaggtaaaaggcacaaacattttac 1193
                                              gatggatttaaggcaacttctcaaaaagccaactttcgactctgaaacggagctttggaa 1250
                                                                            1434 cgcgaggattcggaggttcgtaggtgttgagaaaagtggagataaatcgagttcgatgga 1493
                                                                                                                                                                                     1494 aaagaagcaacaatggaagaagaataatttgagacttagtttttcgaaaagaatgtatga 1553
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/note= "antisense oligonucleotide (Claim 12)"
complement (301..350)
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/note- "antisense oligonucleotide (Claim 12)"
complement (51..100)
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/note= "antisense oligonucleotide (Claim 12)"
complement (151..200)
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/notc= "antisense oligonucleotide (Claim 12)"
complement (251..300)
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/note= "antisense oligonucleotide (Claim 12)"
complement (101..150)
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'note= "antisense oligonucleotide (Claim 12)"
                                                                                                                                                                                                                                                                                                                     ACC synthase; 1-aminocyclopropane-1-carboxylate synthase; ethylene; transgenic plant; wilting; geranium; pPHSacc44; ss.
                                                                                                                                                                                                                                                                                                      Pelargonium 1-aminocyclopropane-1-carboxylase synthase cDNA
                                                                                                                                                                                                             tgatatcaccatgtcacctcactctccc 1507
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                                                                                                                                                                                                                                                                                                                                            Pelargonium x hortorum cv. Sincerity.
                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
39.1487
/*tag= a
1849..1854
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2635..2640
/*tag= c
complement (1..50)
                                                                                                                                                                                                                                                          AAV30325 standard; cDNA; 2678 BP
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This cDNA clone, designated pPHSacc44 (ATCC 98178), codes for a 54.2 kDa 1-aminocyclopropane-1-carboxylate synthase (ACC synthase) (see AAW6024) of geranium (Pelargonium x hortcrum cv. Sincerity). High quality mRNA was obtained from flower tissue using a novel adaptation of the 2-butoxyethanol precipitation technique. This was converted to cDNA and screened with a probe generated by PCR amplification (see AAV30328-29). The PPHSacc44 (see AAV30328-29). The PPHSacc44 (see AAV30326), and rose ACC synthase cDNA clone pRsacc40 (see AAV3030), are also claimed. These ACC synthase genes, or their (see AAV3030), and missense orientation under control of a strong promoter, can be used to genetically modify a plant, especially geranium, rose or woody plant. As a consequence, the amount of ACC synthase produced in the plant cells is reduced and the rate of ACC conversion to ethylene decreases. This can be used to prolong the shelf-life of cut flowers and to reduce leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated ACC synthase genes - are obtained from geranium and rose, used to develop products for producing plants with reduced ethylene levels, for increasing shelf-life
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/note= "antisense oligonucleotide (Claim 12)"
complement (351..400)
                                                                                 (Claim 12)"
                                                                                                                                   /*tag= 1
/note= "antisense oligonucleotide (Claim 12)"
complement (451..500)
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/note* "antisense oligonucleotide (Claim 12)"
complement (1..2678)
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                                                 /*tag= k
/note= "antisense oligonucleotide
complement (401..450)
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ilarity 66.6%; Pred. No. 1.6e-170;
Conservative 0; Mismatches 455;
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P-PSDB; AAW60234.
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                                                                                                                                                                                                                                                                                                                                                                        caacacagactcagtatcttttagcatcgatgctaaatgatgatgaggtttgtggagaggt 1081
                                                                                                                                                                                                                                              841
                                                                                                                                                                                                                                                           724 acatecacetagicategaegaaatetaegeegeeaeegittiegeegeeeeggagiteg 783
                                                                                                                                                                                                                                                                                           843
                                                             taggcacaatcatggacagaaagacactgagaacogtggtgagcttcatcaatgagaagc 781
                                                                                                                                                                                                                                                                                                          acattgtttatagtctttcaaaggacatggggttccctggcttcagagtcggcatcatat 961
                      gtatccaccttgtatgtgatgaaatatatgctgcaacagttttcagccaacccggtttca
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                                                                                                                                                                                                                                                                                                                   actettacaatgatgetggttaattgtgcacgcaaaatgtcaagetttggattggtgt
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                                                      gaaacagaatcacgtttgaccctgaccgtattgtcatgagcggtggagccaccggagcac
                                                                                     acgaagtcactgccttttgtttggcagatcccggcgaggcattcttagtgcccattccct
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                                                                                                                                                 602 tgtgcgatagctcaaataatttcgtgttgacaaaggaagcattggaagatgcctatgaga
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2 DNA sequences (AAT66246-47) respectively code for 1-aminocyclopropane carboxylase synthases (ACC synthase) GAC-1 (AAW09878) and GAC-2 (AAW09879), enzymes involved in the biosynthesis of ethylene in plants. In a method for the commercial production of transgenic plants, Agrobacterium vectors carrying antisense of ECC synthase or ACC cxidase (see also AAT66248) are used to inoculate petiole explants of a mother plant, pref. Pelargonium x domesticum. The resulting callus is cultured and used to regenerate transgenic plants. The antisense genes prevent formation and fruit ribening.
105 tgtcaaagattgcaaccaacgacggacacggcgagaactccccatatttcgatggttgga 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACC synthase; 1-aminocyclopropane-1-carboxylate synthase; antisense; ethylene; transgenic plant; Pelargonium x domesticum; in vitro propagation; tissue culture; ripening; ss.
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                                               1442 gtaacttgaggctgagcctcaaaaccagaaggtttgatgatatcaccatgt 1492
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Pred. No. 3.9e-170;
0; Mismatches 456; Indels
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/*tag= a
/transl_except= 821..823:_aa:Pro
/note= "TTC codes for Phe"
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Best Local Similarity 66.5%;
Matches 912; Conservative 0
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Search completed: August 21, 2002, 02:07:21 Job time: 9562 sec

Comparison (15) Comparison	Sequence 1, Appli Sequence 3, Appli Sequence 14, Appli Sequence 7, Appli Sequence 7, Appli Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli	USE IN PLANTS	; Indels 18; Gaps 2; ccccatactttgatggat 178
August 20, 2002, 23:24.09 Search time 96.17 seconds 32 32 32 32 32 32 32 3	1384 9614 159 2 7218 800 2 800 2 1400 1 1701 3 1701	SE GENE AND ITS I, SUITE 2200 1.0, Version #1 5,107 01170 ore 735; DB 1;	rity 70.8%; Pred. No. 1.55-119 nservative 0; Mismatches 40C agatggctattggggatggacatggcgaatcat
CenCorre version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. August 20, 2002, 23:24:09; Search time 96.17 Secon (without alignments)	28 30 31 31 31 31 31 31 31 31 31 31	1 1 6 nc 1, Appl nt No. 57679 n	Best Loc Matches 119
	GenCore version 4.5 copyright (c) 1993 - 2000 Compugen Ltd. nucleic search, using sw model August 20, 2002, 23:24:09; Search time 96.17 Secon (without alignments) 10S-09-763-957-1 e: 1923 1 atcctctcccacttacttaggtcttcaaattcatttc e: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 383533 seqs, 122816752 residues	ag length: 0 ag length: 0 ag length: 2000000000 Ing: Minimum Match 100% Listing first 45 summaries Issued_Patents_NA:*	15.8 994 2 US-08-860-577-7 Sequence 7, 14.4 7587 4 US-08-378-313-22 Sequence 22 14.3 9060 4 US-08-378-313-20 Sequence 20 13.5 1743 4 US-09-171-482-1 Sequence 1,

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Sequence 3, Application US/08724194

Patent No. 5824875

GENERAL INFORMATION:
APPLICANT: RANU, RAJINDER S.
TITLE OF INVENTION:
TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS;
TITLE OF INVENTION: 1N GERANIUMS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: SANTANGELO LAW OFFICES PC
STREET: 315 WEST OAK STREET, STE 701
CITY: FOR COLLINS
STATE: CO
COUNTRY: USA
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                              1379 tccgcaactttgtgcttcaaaacaaggaggtcgtggtgtctaataagaaacattgttggc 1438
1122 TGCGTAGACTGCTGAAAGAACAGACATTTGAAGCAGAAATGGTGTTATGGAGAGTAATTA 1181
                                                                                                                                                                                                                             1439 acagiaactigaggotgagcotc-----aaaaccagaaggitigatgata 1483
                                                                                                                                                                                                                                                                       1421
                                                                                                                                                                                 167 actttgatggatggaaggcttatgatcaaaacccctttcatcccacagataatcctaacg 226
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                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,194
FILING DATE: 01-OCT-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: SANTANGELO, LUKE
REGISTRATION NUMBER: 31,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 224-3100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1878 base pairs
TYPE: nucleic acid
STRANDENESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-724-194-3
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1265 CTGTGGAGAGTGATAATCAATGAAGTGAAGCTAAATGTGTCGCCAGGGGGCGTCGTTCCAT 1324
                                                                                                                                                 TITLE OF INVENTION: DUALSTRIED PROTEINS, RECOMBINANT
TITLE OF INVENTION: DNA SEQUENCES AND PROCESSES FOR CONTROLLING THE
TITLE OF INVENTION: RIPENING OF COFFEE
CORRESPONDENCE: 13
CORRESPONDENCE ADDRESS:
                                                                               1363 attgetttgeaacgaatecgeaactttgtgetteaaaacaaggaggtegtggtgt----
                                                                                              1418 -ctaataagaaacattgttggcacagtaactt---gaggctgagcctcaaaaccagaagg
                                                                                                                                                                                                                                                                                                                  APPLICANT: STILES, JOHN I.
APPLICANT: MOISYADI, STEFAN
APPLICANT: NEUPANE, KABI R.
TITLE OF INVENTION: PURIFIED PROTEINS, RECOMBINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 673.8; DB 2;
Pred. No. 7.6e-196;
                                                                                                                                                                                     1474 tttgatgatatcaccatgtcacctcactctcccc 1507
                                                                                                                                                                                                   ADDRESSEE: JONES, DAY, REAVIS & POGUE STREET: NORTH POINT, 901 LAKESIDE AVENUE CITY: CLEVELAND STATE: OHLO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 44114
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/695,412B
FILING DATE: 12-AUG-1996
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/485,107
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                            Sequence 11, Application US/08695412B Patent No. 5874269 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: MS-DOS v. 5 SOFTWARE: WordPerfect v. 6.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: GRIFFITH, CALVIN P.
REGISTRATION NUMBER: 34, 831
REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (216) 586-7050
TELEFAX: (216) 579-0212
INFORMATION FOR SEG ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.0%;
68.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
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Best Local Similarity
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Length 2040;

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                                           1282 TICTGGATGGACTTAAGGAGACTCCTCAGGGAGTCCACATTTGAGGCAGAATGGAACTT 1341
                                                                                     1420 aataagaaacattgttggcacagtaacttgaggctgagcctcaaaaccagaaggtttgat 1479
                                                                      1402 TCAGAACCAGGATGGTTCAGAGTTTGCTTTGCCAACATGGACGACGAAGTGTGAGAGTT
                                                                                                                                                                           1366 gctttgcaacgaatccgcaactttgtgcttcaaaacaaggaggtcgtggtg-----tct
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                                                                                                                                                                                                                                                                                                 E: MATHEWS, COLLINS, SHEPHERD & GOULD P.A.
100 Thanet Circle, Suite 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:

APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/043,627
FILING DATE: 20-MAR-1998
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996
PRIOR APPLICATION NUMBER: AU PN5559
FILING DATE: 20-SEP-1995
PRIOR APPLICATION NUMBER: AU PN5559
FILING DATE: 20-SEP-1995
FILING DATE: 02-MAY-1996
ATTORNEY-AGENT INFORMATION:
ANALES DATA:
ANALCATION NUMBER: AU PN9603
FILING DATE: 02-MAY-1996
ATTORNEY-AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 9, Application US/09043627
; Patent No. 6124525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Dernstein, Scott N.
REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 3573
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
TELEFAX: 609-924-8555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1113 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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               atggatttaaggcaacttctcaaaaagccaactttcgactctgaaacggagctttggaaa
                                                                  Sequence 24, Application US/08378313
Patent No. 6207881
GENERAL INFORMATION:
APPLICANT: THEOLOGIS, ATHANASIOS
APPLICANT: SATO, TAKAHIDO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2230;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
FILING DATE:
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.8%; Score 630.2; DB 4;
llarity 65.4%; Pred. No. 1.7e-182;
Conservative 0; Mismatches 493;
                                                                                                                        1312 ccagggtggtttagggtgtgctatgccaacatggatga 1349
                                                                                                                                       1075 CCAGGATGGTTTCGGGTTTGTTTCGCCAACATGGACGA 1112
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REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 21190-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 856-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-ARR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-DOS
                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 706141
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 2230 base_pairs
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Best Local Similarity
Matches 961; Conserv
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US-08-378-313-24
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US-08-378-313-24
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                                                                               Length 1113;
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                                                                             Query Match 33.0%; Score 635.2; DB 3; Best Local Similarity 74.3%; Pred. No. 3.4e-184; Matches 831; Conservative 0; Mismatches 278;
                        1..1113
            CDS
         ; NAME/KEY:
; LOCATION:
US-09-043-627-9
FEATURE
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TELECOMMUNICATION INFORMATION:
TELEFHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
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Best Local Similarity 65.3%;
Matches 959; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1800 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: NUCLEIC ACID
STRANDEDNESS: double
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US-07-809-457A-8
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STATE: M.
COUNTRY:
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                                                               tatgcaaatgggtcttgctgagaatcagcttacctctgatttggttgaagattggatact 290
                                                                           gcccattccctattatccaggctttgaccgggatttgaggtggagaacaggagttaaact
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                               gaacaaccetgaagcetecatttgcaetecagaaggaataaatgattteagggecatage
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                    tgttccagttatgtgcgatagctcaaataatttcgtgttgacaaaggaagcattggaaga
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APPLICATION NUMBER: US/07/809,457A
FILING DATE: 19911217
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Pred. No. 1.4e-181;
O; Mismatches 495;
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APPLICANT: Klee, Harry J.
APPLICANT: Klabore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripening
TITLE OF INVENTION: in Plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Monsanto Co. BB4F
STREET: 70 Chesterfield Village Parkway
CITT: St. Louis
STATE: Missouri
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PRIOR APPLICATION BOOF
PRIOR PAPLICATION DATE: 05 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: HOGENEY Jr., Dennis R.
REGISTRATION NUMBER: 30,914
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPOUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPOUTER: IBM PC COMPATIBLE
COMPOUTER: IBM PC COMPATIBLE
COMPOUTER: IBM PC COMPATIBLE
COMPARE: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/553,943
FILLING DATE:
ONLY 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Moneanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
GTTY: St. Louis
STATE: Missouri
COUNTRY: USA
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REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10538)A
TELECOMUNICATION INFORMATION:
TELEPHONE: (314,537-6099
INFORMATION FOR SEQ. ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-00-553943-8

Sequence 8, Application US/08553943

Patent No. 5702933

GENERAL INFORMATION:
APPLICANT: Klee, Harry J.
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Right NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1554 TGAAAGTGTTTTGTCACCACTTTCGTCAC 1582
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FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
US-08-553-943-8
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LENGTH: 1800 base pairs
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STRANDEDNESS: double
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1554 TGAAAGTGTTTTGTCACCACTTTCGTCAC 1582
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REGISTATION UNBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314,537-604)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1800 base pairs
TYPE: NUCLEIC ACID
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PCT-US91-09437-8
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                             15;
       Length 1800;
      Score 627; DB 1; Length 18
Pred. No. 1.4e-181;
0; Mismatches 495; Indels
       32.6%;
65.3%;
                 Best_Local Similarity 65.3
Matches 959; Conservative
       Query Match
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Fruit Ripening and Senescence COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA: APPLICANT: Kiee, Harry J.
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripeni
TITLE OF INVENTION: In Plants
NUMBER OF SEQUENCES: 17
CORRESSORSE: ADDRESS:
ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway 38-21(10538)A APPLICATION NUMBER: PCT/US91/09437 FILING DATE: 19911217 CLASSIFICATION: 800 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY AGENT INFORMATION:
NAME: HOEFINE JI., Dennis R.

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                                                        Length 1800;
                                                                           Indels
                                                       Score 627; DB 5; L
Pred. No. 1.4e-181;
); Mismatches 495;
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               ; MOLECULE TYPE: CDNA to mRNA PCT-US91-09437-8
                                                      32.6%;
ilarity 65.3%;
Conservative
          linear
                                                                Similarity
STRANDEDNESS:
                                                      Query Match
Best Local Simi
Matches 959;
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APPLICANT: RANU, RAJINDER S.

TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
TITLE OF INVENTION: IN GERANIUMS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
tggattggtgtcaacacagactcagtatcttttagcatcgatgctaaatgatgatgagtt 1070
                                                                                                                                                                                                            tggggggttggccaaagttggcataaagtgcttgcaaagcaatgctggtctatttgtgtg 1190
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STREET: 315 WEST OAK STREET, STE 701
CITY: FORT COLLINS
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FILING DATE: 01-OCT-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-724-194-2; Sequence 2, Application US/08724194; Patent No. 5824875; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION
TELEPHONE: (970) 224-3100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2678 base pairs
TYPE: nucleic acid
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NAME: SANTANGELO, LUKE
REGISTRATION NUMBER: 31,9
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REGISTRATION NUMBER: 31,997 TELECOMMUNICATION INFORMATION:
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66.5%;
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NAME: SANTANGELO, LUKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1945 base pairs
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STRANDEDNESS: double
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Best Local Similarity
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US-08-724-194-1
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COUNTRY: US
ZIP: 80521
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                                                                                                                                         aggettatgateaaaacecettteateeeagataateetaaeggtgttatgeaaatgg 241
                                                                                                  Gaps
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                                                                                                                                                           124 AGGCTTATGACCGTGATCCGTTCCATCCGTCTCAGAATCCTAACGGTGTTATCCAGATGG
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                                                                                .,
                                                            Length 2678
                                                                              Indels
                                                         32.6%; Score 627; DB 1; L. 66.6%; Pred. No. 1.8e-181; L. 1ve 0; Mismatches 455;
                     DNA (genomic)
                                                                             913; Conservative
           linear
                                                                     Similarity
       ; TOPOLOGY: 1in
; MOLECULE TYPE:
US-08-724-194-2
STRANDEDNESS:
                                                          Query Match
Best Local S:
Matches 913,
                                                                                                  122
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APPLICANT: RANU, RAJINDER S.
TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE
TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
TITLE OF INVENTION: IN GERANIUMS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                  1081 AGGACTIGGGGATIGGGTGTTTAAAGAGCAACGCGGGCTCTACTICTGGATGGATITGC 1140
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,194
FILING DATE: 01-OCT-1996
CLASSIFICATION: 800
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Pred. No. 4.6e-181;
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315 WEST OAK STREET, STE 701
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                    ggcaacttctcaaaaagccaactttcgactctgaaacggagctttggaaagttatcattc 1261
                                                                              atgaagttaagatcaatgtttcacctggctattccttccattgcactgagccagggtggt 1321
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No. 5.8e-168;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/POCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/378,313
                                                                                                                                                                                                                                                                                                                                                                      Sequence 18, Application US/08378313
Patent No. 6207881
GENERAL INFORMATION:
APPLICANT: THEOLOGIS, ATHANASIOS
APPLICANT: SATO, TAKAHIDO
TITLE OF INVENTION: GENETIC CONTROL
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
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Pred.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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(415) 494-0792
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66.4%;
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LENGTH: 1703 base pairs
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INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: sing
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Best Local Similarity
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US-08-378-313-18
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Conservative
912;
Matches
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                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: BIRD, COLIN R
APPLICANT: FLETCHER, JONATHON D
TITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/632,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.7%; Score 571.4; DB 2;
64.1%; Pred. No. 1.3e-164;
.ive 0; Mismatches 501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTAATION NUMBER: 16,773
REERENCE/DOCKET NUMBER: 223355/SEE50112/US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 861-3000
                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CUSHMAN DARBY AND CUSHMAN STREET: 1100 NEW YORK AVENUE N.W.
                                                                                                                                                                                                             1305 ATAGCTTTGTCGAAAACATCGACAAG 1330
                                                                                                                                                                                  1382 gcaactttgtgcttcaaaacaaggag 1407
                                                                                                                                                                                                                                                                                Sequence 1, Application US/08632598 Patent No. 5886164
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Floppy disk
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ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
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Best Local Similarity
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CLONE: ACS GENE
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MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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APPLICANT: FLETCHER, JONATHON D
ITLE OF INVENTION: RIPENING-RELATED GENES FROM BANANA
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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Pred. No. 1.3e-164;
D; Mismatches 501;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY AND CUSHMAN
STREET: 1100 NEW YORK AVENUE N.W.
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REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 861-3000
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Best Local Similarity 64.1%;
Matches 914; Conservative C
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER: US,
FILING DATE:
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TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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PRIOR APPLICATION DATA:
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ZIP: 20005-3918
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CLONE: ACS GENE
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COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUTER TYPE: ELOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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APPLICANT: Botella, Jose Ramon
TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: MATHEWS, COLLINS, SHEPHERD & GOULD
STREET: 100 Thanet Circle, Suite 306
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APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996
APPLICATION DATA:
APPLICATION NUMBER: AU PN5559
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA:
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FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09043627
Patent No. 6124525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Bernstein, Scott N.
REGISTRATION NUMBER: 38,827
REFERENCE/DOCKET NUMBER: 355
TELECOMMUNICATION: TELECHONE: 609-924-8555
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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MOLECULE TYPE: CDNA
FEATURE:
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COMPUTER: IBM PC COMPETIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FPILICATION NUMBER: US/09/043,627
FILING DATE: 20-MAR-1998
CLASSIFICATION: 800
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Pred. No. 1.3e-163;
); Mismatches 317;
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TITLE OF INVENTION: NOVEL ACC SYNTHASE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSILLCATION: OVER PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU96/00591
FILING DATE: 20-SEP-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU PN5559
FILING DATE: 20-SEP-1995
PRIOR APPLICATION DATA: APPLICATION DATA: NOFICATION NUMBER: AU PN9603
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: BELINGLATION NUMBER: AU PN9603
FILING DATE: 02-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: BELINGLATION NUMBER: 38, 38, 327, 1110
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                                                                                                          Sequence 7, Application US/09043627
Patent No. 6124525
GENERAL INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-924-8555
                                                                                                                                                                                                                                                                                      ADDRESSEE: MATHEWS, COLLINS
STREET: 100 Thanet Circle,
CITY: Princeton
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70.4%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                   Length 1104;
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                                                                   2; DB 3;
1.2e-164;
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Pred. No. 1.2e-
0; Mismatches
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ilarity 71.6%;
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Matches 792; Conserv
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: August 20, 2002, 22:51:49; Search time 3456.34 Seconds (without alignments) 7509.286 Million cell updates/sec Title: US-09-763-957-1 Perfect score: 1923 Sequence: 1 atcctctcccacttacttaggtcttcaaattcattcc 1923 Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0 Searched: 13736207 seqs, 6748477542 residues Total number of hits satisfying chosen parameters: 27472414 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Listing first 45 summaries Database : EST:* 1: em_estba:* 3: em_esthum:* 4: em_estin:* 5: em_estin:* 6: em_estpl:* 7: em_estrov:* 8: em_htc:* 9: gb_est2:* 11: gb_htc:*	12: gb_gss:* 13: em_gss_hum:* 14: em_gss_hum:* 15: em_gss_lnv:* 16: em_gss_lnv:* 17: em_gss_lnv:* 18: em_gs_	c 1 496.6 25.8 799 10 B1970666 BH970666 CM830011A 2 486.8 25.3 578 9 ARA58572 ARA488572 ARA488572 ARA488572 ARA488572 ARA488572 ARA488572 ARA488572 ARA488572 Sh10002.y ARA58672 ARA5867 ARA58672 ARA5867 ARA5867

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/clone_lib="Gm-ri083"
/note="The library Gm-ri083 is a sequence-driven, reracked set of 4,992 clones selected from Chall Librarias from various tissues and stages of development of soybean. It represents 1117 sequences from the progenitor library Gm-cl099 (from mature roots of 2 month old greenhouse grown 'Williams' soybean plants); 820 sequences from the progenitor library Gm-cl013 (from 2 to 3 week old whole plants of Williams); and 3055 sequences from the plants of Williams); and 3055 sequences from the plants of Williams); and 3055 sequences from the clark Stacey). The 5' ESTS of the source clones from the different progenitor libraries was used to select singletons, or a representative of each contig, which were reracked to form library Gm-ri083. The cONA clones of the reracked Cm-ri083 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ennest Retzel, Center for Computational Genomics and Bloinformatics, University of Minnesota, http://www.lncyte.com, and 3' sequencing by the Reck Center for Comparative and Bloinformatics, St. Louis, http://www.incyte.com, and 3' sequencing by the Reck Center for Comparative and Functional Genomics, University of Illinols, http://www.lncyte.com, and 3' sequencing by the Reck Center for Comparative and Functional Genomics, Of Illinols, http://www.lncyte.com, and 3' sequencing by the Reck Center for Comparative and Functional Genomics, Conter for Comparative and Functional Genomics and Co
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Pred. No. 3.3e-113;
0; Mismatches 125; Indels
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Best Local Similarity 81.3%;
Matches 642; Conservative
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E 1 (bases 1 to 578)
Shoemaker, R. Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marrah, T., Hiller, L., Kucaba, T., Marth, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Materston, R. and Wilson, R.

In Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anote—"Voctor: pBluescript II XR; Site_1: EcoRI; Site_2: XhoI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were innoculated with Bradyrhizoblum japonicus, strain USDAINO priot to harvest. Stratagene's CDNA synthesis Kit (catalog number 200401) was used to synthesize the CDNA. First-strand synthesis was performed
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Fax: 314 286 1810

South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com

Insert Length: 3902 Std Error: 0.00

High quality sequence stop: 390.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE020529 mRNA linear EST 03-DEC-2001 sm44h02.91 Gm-c1028 Glycine max cDNA clone GBNOME SYSTEMS CLONE ID: Gm-c1028-6796 5' similar to SW:1ALC_SOYBN P31512.

1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                ggcatcacaatccagtgtcctacaagttgtgctgcttcatgcac 1737
                                                                                                                                                                                                             141
                                                                                                                                                                                                                                                                                                                                                       81
                                                           260 Trgtraccaacarcgaagreferrecerrecercaragaactrgferacregaaacar
                                                                                                                                      gccccttcaatcttagggg----catttttttttttttcacttaccaaa----ggttc
                                                                                                                                                                               200 GCCCCTTCAATTTTTAGGGGCATTTTTTTTTTTTTTTCACTTACCAAATAATGGGTTC
                                                                                                                                                                                                                                                                                                                      /clone="GENOME SYSTEMS CLONE ID: Gm-c1028-6796"
/clone_lib="Gm-c1028"
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/lab_host="DH10B"
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/db_xref="taxon:3847"
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hemimethylated. A modification of Stratagene's hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (VaA,C, or G) was added to the 3' end of the primer [GAGAGAGAGAGACACTAGTCTCCAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's spluescript II SR(+) that has been digested with EcoRI and XhoI, and phosporylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Reim and Dr. Virginia Coryell.
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5-methyl dCTP, hence the ligated cDNA was nethylated. A modification of Stratagene's
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 486.8; DB 9;
Pred. No. 8.5e-111;
0; Mismatches 57;
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llarity 90.1%;
Conservative C
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Best Local S
Matches 521
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ORIGIN
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RESULT AW458572

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Localini/Qualifies

1. .536

/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1016-4396"
/clone_lib="Gm-c1016"
/tissue_type="immature flowers of field grown plants"
/tissue_type="immature flowers of field grown plants"
/lab_nost="xilo-Gold"
/note="Vector: pBluescript II XR; Site_l: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from immature flowers of field grown plants. The cDNA
library was prepared using the Stratagene pBluescript II
XR library construction kit. Complementary DNA was
synthesized from mRNA using a primer consisting of a poly
(dT) sequence with a XhoI restriction site. EcoRI adapters
were ligated to the blunt-ended cDNA fragments followed by
XhoI digestion. The cDNA fragments were directionally
cloned into the EcoRI-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into Xilo-Gold host cells. This library was
constructed by Dr. Randy Shoemaker and Dr. John
                                                                                                                                                                                                                                                                                                                                                                                  Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Thelsing, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, M., Schurk, R., Materston, R., and Wilson, R., Materston, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R., Grackson, Y., Cardenas, M., McCann, Public Soybean Est Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com Insert Length: 1062 Std Error: 0.00 Seq primer: -40RP from Glaco High quality sequence stop: 427.
AW458572 BT 03-DEC-2001 S160bQ. Thear Linear EST 03-DEC-2001 Sh10bQ.yl Gm-c1016 Glycine max cDNA clone GRNOME SYSTEMS CLONE ID: Gm-c1016-4396 5' similar to SW:1AlC_SOYBN P31531 L-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                     Phaseoleae;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae,
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Pred. No. 1e-101;
0; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
                                                                                                                                         GI:7028789
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91.0%;
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AW458572.1
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BASE COUNT 207 a 83 c 147 g 210 t 4 others ORIGIN	Query Match 20.6%; Score 396.2; DB 10; Length 651; Best Local Similarity 77.7%; Pred. No. 3.7e-88; Matches 505; Conservative 0; Mismatches 136; Indels 9; Gaps 2;	Qy 853 gagatattagaggatgaaacagacatagagtgtgaccgcaacctcgtacacattgtttat 912 	Qy 913 agtotttoaaaggacatggggttocotggottoagagtoggoatcatatactottacaat 972 	Oy 973 gatgctgtggttaattgtgcacgcaaaatgtcaagctttggattggtgtcaacacagact 1032 	<pre>Qy 1033 cagtatcttttagcatcgatgctaaatgatgatgtttgtggagaggtttctggcagag 1092 </pre>	Oy 1093 agtgcaaagagttggctcaaaggttcagggttttcactggggggttggccaaagttggc 1152 	Oy 1153 ataaagtgcttgcaaagcaatgctggtctatttgtgtggatgga	<pre>Qy 1273 atcaatgtttcacctggctattccttccattgcactgagccagggtggtttagggtgtgc 1332 </pre>	Oy 1333 tatgccaacatgatgatatggctgtgcaaattgctttgcaacgaatccgcaactttgtg 1392 	Oy 1393 cttcaaaacaaggaggtcgtggtgtctaataagaaacattgttggcacagt 1443	Oy 1444 aacttgaggctgagcctcaaaaccagaaggtttgatgatatcaccatgtc 1493 	RESULT 5 B1974504 LOCUS B1974504 507 bp mRNA linear EST 30-NOV-2001 DEFINITION Sa169409, yl Gm-c1068 Glycine max cDNA clone SENOME SYSTEMS CLONE		KEYWORDS EST. SOURCE SOYbean. ORGANISM Glycine max Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		REFERENCE 1 (Dases 1 to 507) AUTHORS Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna AUTHORS Shoemaker,R., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., A., Bolla,B., Marra,M., Steptoe,M., Theising,B., Allen,M., Bowers ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
Qy 1125 tttcactgggggttggccaagttggcataaagtgcttgcaaagcaatgctgtctatt 1184 	Oy 1185 tototogatgtattaaggcaacttctcaaaaagccaactttcgactctgaaacggagct 1244	Oy 1245 tiggaaagttaicattcatgaagttaagatcaaigtttcacctggctattccttccattg 1304 11111	Oy 1305 cactgagccagggtgtttagggtgtctatgccaacatggatgatatggctgtgcaaat 1364	Oy 1365 tgctttgcaacgaatccgcaactttgtgcttcaaaacaaggagtcgtggtgtctaataa 1424	Oy 1425 gaaacattgttggcacagtaacttgaggctgagcctcaaaaccagaaggtttgatgatat 1484	Oy 1485 caccatgtcacctcactcacctcagtcacctatggttaa 1529	RESULT 4 BF649567 LOCUS LOCUS DEFINITION NF0799012C1F1099 Elicited cell culture Medicago truncatula cDNA ACCESSION BF649567	VERSION BF649567.1 GI:11914697 KEYWORDS EST. SOURCE Darrel medic. ORGANISM Medicago fruncatula Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Spermatophyta; Magnollophyta; eudicotyle Rosidae; eurosids I; Fabales; Fabaceae; Medicago. 1 (bases 1 to 651)	AUTHORS Torres Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. TITLE Expressed Sequence Tags from the Samuel Roberts Noble Foundation -	JOURNAL Unpublished (2000) COMMENT Contact: Dixon RA Plant Biology Division The Samuel Roberts Noble Foundation		FEATURES Source 1		/tissue_type="Cell cultures derived from root tissues" /dev_stage="Cell suspensions were subcultured every 14 days. Cells were induced six days after subculture"	/note="vector: Lampda Zap; Cells were induced with yeast cell wall extracts equivalent to 50ug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."

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260
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BM412805
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,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Materston,R. and Wilson,R.
Public Soybean EST Project
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccuêresgen.com
High quality sequence stop: 357.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Anote-"Vector: pBluescript II SR+; Site_I: ECORI; Site_2:
XhoI: The CDNA library was constructed from mRNA isolated
from drought stressed leaf tissue of the cultivar Williams
82. The month old greenhouse grown plants were deprived of
water for 3 days prior to harvesting the stressed leaf
tissue. Complementary DNA was synthesized from mRNA using
a primer consisting of a poly(dT) sequence with a XhoI
restriction site. ECORI adapters were ligated to the
blunt-ended CDNA fragments followed by XhoI digestion. The
CDNA fragments were directionally cloned into the
ECORI-XhoI restriction site of the pBluescript vector. The
ligated CDNA fragments were transformed into DH10B host
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                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Leaf, drought stressed, 1 month old plants, greenhouse grown"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells (GlocoBL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1240 gagetttggaaagttateatteatgaagttaagatcaatgttteaeetggetatteette 1299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GBNOME SYSTEMS CLONE ID: Gm-c1068-4001"
/clone_lib="Gm-c1068"
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Pred. No. 2.8e-86;
0; Mismatches 59
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88.0%;
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J. (bases 1 to 775)
Alcala, J. Vrebalov, J., White, R., Vision, T., Karamycheva, S.A., Tsal, J., Bougri, O., Kirkness, E., Utterback, T., Van Aken, S., Ronning, C.M., Fraser, C.M., Martin, G.B., Tanksley, S.D. and Giovannoni, J. Generation of ESTs from tomato fruit tissue, breaker stage (2002)
                                                                                                                                                                                                                                                                               EST 22-JAN-2002
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Site_2: XhoI; supplier: Boyce Thompson Institute;
sequencing: The Institute for Genomic Research. Fruit
were harvested at the breaker stage (first sign of
lycopene accumulation on the blossom end of fruit). Fruit
were cut in half and the seeds and locules were discarded
prior to freezing the pericarp."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                    EST587132 tomato breaker fruit Lycopersicon esculentum cDNA clone cLEG61011 5' end, mRNA sequence.
BM412805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              528 agtgcccattccctattatccaggctttgaccgggatttgaggtggagaacaggagttaa
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Pred. No. 2.7e-78;
0; Mismatches 252; Indels
                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Lycopersicon esculentum"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="clE6661011"
/clone="tomato breaker fruit"
/fissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University Genomics Institute
                                                                                                                                                                                                                                                                               775 bp
                                                                                               1658 gcaataacaggaaattcctgatgttgt 1684
                                                                                                                          ACAATAACAGACACTCCTGATATTGT 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon esculentum
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Best Local Similarity 67.2%;
Matches 519; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unpublished (2002)
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ESTs from roots of Medicago truncatula after inoculation with Phytophthora medicaginis
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Medicago truncatula
Medicago truncatula
Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolleae;
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Minnesota EST name:M251649e ; TIGR sequence name:MTBAW84TK ; More
information, including clone ordering, is available at. .
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                                                                                                                                                                                                                                  CAAAGATTTAGTTCACATCGTCTACAGTCTTTCAAAAGACATGGGGTTACCAGGATTTAG
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                             tccatcaaatccattaggcacaatcatggacagaaagacactgagaaccgtggtgagctt
                                                                                           catcaatgagaagcgtatccaccttgtatgtgatgaaatatatgctgcaacagttttcag
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University of Minnesota
411 Borlawy Hall, 1991 Upper Buford Circle,
TTE1: 612 625 5715
Fax: 651-649-5058
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Contact: Carroll P. Vance
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AW560294.1 GI:7205720
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/dev_stage="roots harvested at 10 days post inoculation with Phytophthora medicaginis"
/lab.host="E. coli strain XLOLR"
/lab.host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI: Site_2: XhOI; cDNA was prepared from polya+ enriched RNA from roots harvested at 10 days post inoculation with Phytophthora medicaginis. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells. Note: EST may be of fungal origin."
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6
                                                                                          /cultivar-"genotype A17"
/db_xref='taxon:3880"
/clone="pbSIR-26N23"
/clone_lib="bSIR"
/rissue_type="roots infected with Phytophthora medicaginis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 623;
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                  gAT CC)
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                                                                          /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 197 t
                    Seq primer: SKmod (CTA gAA CTA gtg
Location/Qualiflers
http://chrysie.tamu.edu/medicago
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Best Local S:
Matches 457,
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/note="Vector: pBluescript II SK+; Site_I: EcoRI; Site_2:
XhoI; The CDNA library was constructed from mRNA isolated
from unexpanded leaves and the shoot tips of 2 week old
seedling from the cultivar Williams. The 2 week old
seedlings were salt stressed in a solution of 500mM NaCl
for 3 days prior to harvesting. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments were
transformed into DHIOB host cells (GibcoBRL). This library
was constructed in the laboratory of Dr. Randy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: estéwatson wustl.edu
This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 421.
                                                                                                                                                                                                                                                                                                                                                                                        Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Viderwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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                                                         EST 30-NOV-2001
SYSTEMS CLONE
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="Leaf and shoot tip, salt stressed, 2 week old seedling" /lab_host="DH10B"
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Fax: 314 286 1810
                                                 BM095045

BM095045

BM10525166.y1 Gm-c1066 Glycine max cDNA clone GENOME SYSTEMS CIDE. Gm-c1066-3732 5' similar to SW.1AlC_SOYBN P31531

1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1066-3732"
/clone_llb="Gm-c1066"
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Pred. No. 2.1e-76;
0; Mismatches 50; Indels
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Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 t
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88.3%;
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/ Object = "NF102B06EC"
//Clone="NF102B06EC"
//Clone="Nector: Lambda Zap; Cells were induced with yeast cells ware endouced six days after subculture"
//NOCE="Nector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to Soug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation."

86 a 115 c 121 g 205 t 3 others
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (Bases I to 610)
1 (Chass I to 610)
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                                        gcatattcctctgaatcgtttagaagaagtaactgatatgtgaagattacttggttcttt 1606
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61 CTGAGCCAGGGTGGTTTAGGGTGTGCCTATGCCAACATGGATGATATGGCTGTGCAAATTG 120
                                                                                                                                                Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USP
Tel: 580 221 7302
Fax: 580 221 7380
Email: radixon@noble.org
Insert Length: 630 Std Error: 0.00
Plate: 102 row: B column: 06
Seq primer: TCACACAGGAAACAGCTATGAC.
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/organism~"Medicago truncatula"
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BF650933.1 GI:11916063
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BM410886
BM410886.1 GI:18262516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. (bases 1 to 766)
Alcala,J., Vebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Bougri,O., Kirkness,E., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Glovannoni,J. Generation of ESTs from tomato fruit tissue, breaker stage (2002) Contact: CUGI
                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                   Lycopersicon esculentum
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Finstitute
Seg primer: T3.
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                                   atgggtttcaaggccatggaccaaactcccttgttgtccaagatggctattggggatgga 147
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                  Indels
Length
                88;
DB 10;
        4e-75;
Score 344; DB
Pred. No. 4e-79
0; Mismatches
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1...766
17.9%;
81.8%;
                395; Conservative
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        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                           tomato.
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Query Match
         Local
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BM410886
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DEFINITION
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/note="Vector: pBluescriptSKmcUadapt; Site_1: EcoRi; Site_2: XhoI; suppler: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freeing the pericarp."
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    esculentum"
                                                                                                                                                                                                                                                                         DB 10;
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Pred. No. 3.8e-73;
0; Mismatches 208;
                                                         fruit"
/organism="Lycopersicon escu-
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEG54P6"
/clone=lib="tomato breaker fi
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
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Best Local Similarity 69.3%;
Matches 472; Conservative C
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228
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/db_xref="taxon:3880" |
/clone="lb="billcited cell culture" |
/clone=lb="billcited cell cultures derived from root tissues" |
/closue_type="Cell cultures derived from root tissues" |
/dev_stage="Cell suspensions were subcultured every 14 |
days. Cells were induced six days after subculture" |
/note="vector: Lambda Zap; Cells were induced with yeast cell wall extracts equivalent to Soug/ml glucose in the final concentration. Samples were taken at 0.5, 1, 12 and 24 hours after induction. Equal amounts of RNA from each time point were pooled and used for mRNA isolation." |
// A a 123 c 118 g 216 t 2 others
                                                                                                                                                                                                                                     Torres-Jezez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation - Center for Medicago Genomics Research Unpublished (2000)
                   EST 20-DEC-2000
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                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                BF648314 . 653 bp mRNA linear EST 20-DEC-2
MF046D07EC1F1061 Elicited cell culture Medicago truncatula cDNA
clone MF046D07EC 5', mRNA sequence.
BF648314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.4%; Score 334.8; DB 10; Length llarity 82.3%; Pred. No. 8.1e-73; Conservative 0; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                          Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .653
/organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                Email: radixon@noble.org
Insert Lengih: 653 Sid Error: 0.00
Plate: 046 row: D column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                    BF648314.1 GI:11913444
                                                                                                                                        Medicago truncatula
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                                                                                                                  barrel medic.
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Fax: 58
Email:
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Best Local S:
Matches 395,
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/organism="Lycopersicon esculentum"
/cultuva="TA496"
/db_xref="taxon:4081"
/clone="cLED31P17"
/clone=llb="tomato ovary, TAMU"
/tissue_type="carpel"
/dev_stage="5 days pre-anthesis to 5 days post-anthesis"
/lab_host="XL1-Blue MRF,"
/note="Yector: pBlueScript SK(-); Site_1: EcoRl; Site_2:
xhol; cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lamda ZAP II with 5'
and 3' ends located at the EcoRl and xhol sites,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Asternacy,
Lycopersicon.

1 (bases 1 to 672)

Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E.
Alcala,J., Vrebalov,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Glovannoni,J.
Generation of ESTs from tomato carpel tissue
Unpublished_(1999)
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                                                                                                                                                                                                                                                                                                  EST 18-MAY-2001
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae, euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                             AI898099 ' 672 bp mRNA linear EST 18-MAY-2
EST267542 tomato ovary, TAMU Lycopersicon esculentum cDNA clone
CLED31P17, mRNA sequence.
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                                                                  10 TITGAICCAGAAAGAAIAGITAIGAGIGGAGGAGCAACAGGAGCICAIGAAAGIIIGGCA
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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Pred. No. 5.7e-70;
0; Mismatches 202;
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68.9%;
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AI898099.1
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Page 10

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//did_nost=_Uniost=_DiluserriptII SK+; Site_1: EcoRI; Site_2:
XhoI; This cDNA library was constructed from mRNA isolated
from etlolated hypocotyl tissue of 9-10 day old seedlings
of the cultivar Williams 82. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) primer with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
fragments were ligated to the blunt-ended cDNA fragments
fragments were directionally cloned into the EcoRI. XhoI
restriction site of the pBluescript vector. The ligated
cDNA fragments were transformed into DH10B host cells
(Gibco BRU, This library was constructed by Dr. Randy
Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        575 bp mRNA linear EST 18-MAY-2001 EST243120 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED2N19, mRNA sequence.
                                                                                  /db_xref="taxon:3847"
/clone="GRNOME SYSTEMS CLONE ID: Gm-c1045-267"
/clone="lb="Gm-c1045"
/tissue_type="type="type"typecotyl, 9-10 day old etiolated seedlings"
/lab_host="DH10B"
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Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta; eudicotyledons; core eudicots;
Asteridae, euasterida I; Solanales; Solanaceae; Solanum;
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Pred. No. 9.3e-70;
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   Location/Qualifiers
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Publison, R. and Wilson, R.
Gunpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memortal Parkway Huntsville, AL 35801 For further information
call: (8001-533-4363 or contact via email: ccu@resgen.com
Insert Length: 913 Std Error: 0.00
High quality sequence stop: 434.
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                           /organism="Lycopersicon esculentum"
/cultivar="TA496"
/du_tref="taxon:4081"
/done="ciab2N19"
/clone="lib="tomato ovary, TAMU"
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/tissue_type="carpel"
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/dab_host="XL1-Blue MRF"
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Xhol; cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lamda ZAP II with 5'
and 3' ends located at the EcoRl and Xhol sites,
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I.E., Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni,J. Venter,G.C., Martin,G.B., Tanksley,Generation of Esrs from tomato carpel tissue
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                                                                                                                            Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
1. 575
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Pred. No. 2e-69;
0; Mismatches 158; Indels
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Local Similarity 72.5%;
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
1. .819
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                                                           EST532633 tomato callus, TAMU Lycopersicon esculentum cDNA clone cLEC68H15 5' end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. (bases 1 to 819)
Alcala,J., Vrebalov,J., White,R., Matern,A.L., Vision,T., Holt,I., Liang,F., Upton,J., Craven,M.B., Bowman,C.L., Ahn,S., Ronning, C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Glovannoni,J. Generation of ESTs from tomato callus tissue
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aaaatgtcaagctttggattggtgtcaacacagactcagtatcttttagcatcgatgcta 1056
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llarity 63.5%; Pred. No. 3.8e-68;
Conservative 0; Mismatches 288; Indels 12;
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                                         715 ATTGCTGCTATTAAGAAACAATGCAGCAGGAGAAACTTCAGATCAGCTTATCGTTTCGA 774
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phillips,A.T.
Identification and characterization of a full-length cDNA encoding for an auxin-induced 1-aminocyclopropane-1-carboxylate synthase from etiolated mung bean hypocotyl segments and expression of its mRAA in response to indole-3-acetic acid plant Mol. Biol. 20 (3), 425-436 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 1923)
Botella,J.R., Arteca,J.M., Schlagnhaufer,C.D., Arteca,R.N. and
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V.radiata mRNA for ACC synthase.
11613 347557
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1-amlnocyclopropane-1-carboxylate synthase; ACC synthase.
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AB03346
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 (without alignments) 7433.080 Million cell updates/sec
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Arteca, R. N.
Direct Submission
Submitted (24-JAN-1992) Richard N. Arteca, Department of the Pennsylvania, State University, 103 and 1010 your of the Pennsylvania, State University, 103 and 1010 your of the Park, PA, 16802, USA
Location/Qualifiers

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Nucleotide sequence of soybean ACC synthase
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163. .1617
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Submitted (29-UN-1992) N. Li, U
BARC West, Beltsville MD 20705,
Chases 1 to 1789)
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V.radiata mRNA for 1-aminocyclopropane-1-carboxylate synthase
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                   Identification and characterization of a full-length cDNA encoding for an auxin-induced 1-aminocyclopropane-1-carboxylate synthase from etiolated mung bean hypocotyl segments and expression of its mRNA in response to indole-3-acetic acid Plant Mol. Biol. 20 (3), 425-436 (1992)
 ATCTTTTAGCATCAATGCTAAATGATGATGAGTTTTGTGGAAAGTTTTCTGGTAGAGAG 1171
                                                        atgittcacctggctattccttccattgcactgagccagggtggtttagggtgtgctatg 1336
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                                                                                                                                                                                                                                                                                                                                        1-aminocyclopropane-1-carboxylate synthase.
Vigna radiata
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Z11562.1 GI:22067
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/codon_start=1
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RNLVHITYSJSKANGGPEGFRGIIYSYNDAVYPCSOPGFISIABILEDETDIECD
DEFYERELAESARKLAQRFRVFTGGLAKVGIKCLQSNAGLEVWMDLRQLKKPTFDSE
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Pred. No. 9.6e-273;
0; Mismatches 2;
/organism-"Vigna radiata"
                                                           /tissue_fype="Hypocotyl"
<1. .>1104
/EC_number="4.4.1.14"
                        /cultivar="Berken"
/db_xref="taxon:157791"
/clone="pHIM-1"
               /strain="Rwilcz
                                                                                                                                                                                                                                                                                             57.2%;
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Matches 1101; Conservative
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ESAKRLAQRYRIFTSGLTKVGINCLQSNGGLFVWMDLRGLIKEATLESELELMRVIIH
EVKINVSPGVSFHCSEPGWFRVCYANMDDRDVQIALQRIRSFVVQNNKEVMVSEKNTK
PCWHSNLLSLKTRREDGINFSPFSPFPGSPLVKATT"
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                                                                                                         1; DB 8;
1.4e-243;
tes 307;
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                                                                                                         Query Match 51.3%;
Best Local Similarity 79.0%;
Matches 1217; Conservative
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PQGVIQMGLAENQLTADLVQNWIMSNPEASICTLEGYHNFKEMANFQDYHGLPEFRNA
VAKFWSRTRGNRVTFDDDRIVWSGGATGAHEATFCLADPGDAELVPTPYPGFBDDL
RWRTGVKLVPYICESANNFKITKQAHEAYERATENIRIKGLLITHPSNPLGTYMDR
NTLRTVVRINEKRIHLISDEIXAATVESHPSFISIAEILEHPUPDIEGDRNLVHIVYS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Kosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolleae;
Medicago.
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/protein_id="AAL35745.1"
/db_xref="G1:17266328"
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                                                     atcatatactcttacaatgatgctgtggttaattgtgcacgcaaaatgtcaagctttgga
                                                                                                                                                                                       GAGAGGTTTCTGGCAGAGAGTGCAAAGAGGTTGGCTCAAAGGTTCAGGGTTTTCACTGGG
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mRNA, complete cds.
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Engstrom, E.M. and Long, S.R.
Direct Submission
Submitted (13-NOV-2001) Biological Sciences,
371 Serra Mall, Stanford, CA 94305-5020, USA
Location/Qualifiers
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/cultivar="Jemalong A-17"
/db_xref="taxon:3880"
162. 1625
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PYMHSNLIKJSKRPTDDIMMSPHSFIPQSPLVKATT"
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                                                                                 Location/Qualifiers
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              Peck, S.C. and Kende, H. Direct Submission Submitted (30-UL-1997) M. State University, Plant Bi 48824-1312, USA
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138. .1601
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Peck, S.C. and Kende, H.
Differential regulation of genes encoding
1-aminocyclopropane-1-carboxylate (ACC) synthase in etiolated pea
sedlings: effects of indole-3-acetic acid, wounding, and ethylene
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Submitted (16-NOV-1999) Takeo Harada, Hirosaki University, Facul
Submitted (16-NOV-1999) Takeo Harada, Hirosaki University, Facul
of Agriculture and Life Science; Bunkyoucho 3, Hirosaki, Aomori
036-8561, Japan (E-mail: tharada@cc.hirosaki-u.ac.jp,
Tel:81-172-39-3777, Fax:81-172-39-3750)
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Pred. No. 8.1e-195;
0; Mismatches 384;
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/db_xref="taxon:3750"
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81. .1544
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Malus domestica MdACS-5A
Synthase, complete cds.
AB034992.1 GI:7209850
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Sunako,T., Ishikawa,R.,
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S Populus nigura L. (poplar)

N JP 1997075088-A/1

D 25-MAR-1997

F 07-SEP-1995 JP 1995254510

I HOYA IZUMI, KITANI SHIGEKAZU

C C12N15/09,C07H21/04,C12N9/68//A01H5/00,(C12N9/88,C12R1:19); CC

C topology: Linear;

C topology: Linear;

C hypothetical: No;
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HOYA,I. and Kitani,S.
OZONE-DERIVED 1-AMINOCYCLOPROPANE-1-CARBOXYLIC ACID-SYNTHESIZING
ENZYME GENE GROUP OF WOODY PLANT
PATENT: JP 1997075088-A 1 25-MAR-1997;
TOYOTA MOTOR CORP
cDNA encoding poplar ACC (1-aminocyclopropane-1-carbonic acid) synthetase which is induced by ozone.
E12805.1 GI:3251637
JP 1997075088-A/1.
unidentified
unclassified.
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41.1%; Score 791.2; DB 6;
Best Local Similarity 73.0%; Pred. No. 3.6e-193;
Matches 1047; Conservative 0; Mismatches 378;
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Rebbeck, J. and Davis, K.R.
Direct Submission and Davis, R.R.
Submitted (12-OGT-1999) Nobuyoshi Nakajima, The National Institute
for Environmental Studies, Regional Environment Division; Onogawa
16-2, Tsukuba, Ibaraki 305-0053, Japan (E-mail:naka-320@nies.go.jp,
Tel:81-298-50-2490, Fax:81-298-50-2490)
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/protein_id="BAA94599.1"
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Populus euphratica (cultivar:I-45/51) cDNA to mRNA.
Populus euphratica
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/organism="Populus euphratica"
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ggctt 	ttatc 	rgaag 	TCTG	GGTAC atcce ATCCA ATCCA AGCGI AGCGI	tctta 	aaagt
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GWRTGVOLIPPACDSSNNFYYRAALEAAYERAQKANIRVGGLITNPSNPLGTVLDR
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KDMGFPGRVGIYYZSYNDAVYNCARRASSFGLYSTQYCHLIASMLSDNEFVRRIAGS
KKRKTRHARFTMGLAQVSYNCLKSNGGLFVWMDLRRLLKEOTFEAEWVLWRTIIHEV
KLNVSPGSSFHCPEPGWFRVCFANMDDKTMEVALTRIFTFVLQNKEAIVPRKSNRLWH
SNLALSFQSRRMDDTMMSPCMMSPHTPIPQSPLVRAT"

528 a 371 c 412 g 527 t
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Submitted (16-NOV-1999) Takeo Harada, Hirosaki University, Faculty
Submitted (16-NOV-1999) Takeo Harada, Hirosaki University, Faculty
Of Agriculture and Life Science; Bunkyoucho 3, Hirosaki, Aomori
Off-856i, Japan (E-mail:tharada@cc, hirosaki-u.ac.jp,
Tel:81-172-39-3777, Fax:81-172-39-3750)
Location/Qualifiers
1. 1838
/organism="Malus x domestica"
/db_xref."taxon:3750"
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Malus
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                                                                             two wound responsive genes encoding
1-aminocyclopropane-1-carboxylate synthase in apple. (PGR00-030)
2 (bases 1 to 1838)
Harada,T.
ctttgcaacgaatccgcaactttgtgcttcaaaacaaggaggtcgtggtgtctaataaga 1426
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Sunako,T., Ishikawa,R., Senda,M., Akada,S., Nilzeki,M. and
Harada,T.
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Malus domestica cDNA to mRNA.
Malus x domestica
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                                              31 CATTTAAACAATGGGGTTTACTTTGAGCAACCAACAGCAACTGTTGTCTAAGATAGCAAC
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Length 1838,
               Indels
Score 784; DB 8; I
Pred. No. 2.6e-191;
               0; Mismatches 375;
40.8%;
               Conservative
       Similarity
               Matches 1038;
Query Match
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Rosales; Rosaceae; Maloideae; Pyrus.
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/protein_id="AAL66205.1"
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El Sharkawy, I., Li,Z.G., Latche, A. and Lellevre, J.M.
Direct Submission
Submitted (30-MAY-2001) Biologie Moleculaire et Physiologie Maturation des Fruits, INP - ENSAT, AV. de l'Agrobiopole - B. Castanet Tolosan Cedex, 31326, France
                                                                                                                                tgtttcacctggctattccttccattgcactgagccagggtggtttaggggtgtgctatgc
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El Sharkawy, I., Li, Z.G., Latche, A. and Lelievre, J.M.
Ripening related genes in pear (Pyrus communis)
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/gene="ACS5"
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PLN 26-JAN-2000
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6 (bases 2 to 1734)
7 (citrus alnessis Osbeck) fruit
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Submitted (10-NOV-1998) Wong W.S., Biology, The Hong Kong
University of Science and Technology, Rm.5207, Biology Department,
HKUST, Clear Water By Kowloon, HONG KONG
Location/Qualifiers
         aaagaggttggctcaaaggttcagggtttcactggggggttggccaaagttggcataaa
                                                                                                                          tgtttcacctggctattccttccattgcactgagccagggtggtttagggtgtgctatgc
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/protein_id="CAB60722.1"
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/db_xref="taxon:2711"
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Citrus sinensis.
Citrus sinensis
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TITLE
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                                             Length 1770;
                                                                  Indels
                                           Score 778.6; DB 8;
Pred. No. 6.5e-190;
0; Mismatches 389;
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/translation-"MapalsnqvQllskiaagngggbpypdgwkapesdpyhptkn
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Pred. No. 4.9e-189;
0; Mismatches 393;
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Best Local Similarity 72.3%;
Matches 1066; Conservative
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Carica papaya
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids_II; Brassicales; Caricaceae; Carica.
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2 (bases 1 to 1888)
2 (bases 1 to 1888)
2 (bases 1 to 1898)
Direct Submission
Submitted (28-AUG-1996) Plant Molecular Physiology, College of Tropical Agriculture and Human Resources, University of Hawaii, 3190 Maile Way, St John #503, Honolulu, HI 96822, USA
Location/Qualifiers
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Neupane, K.R., Mukatira, U.T. and Stiles, J.I.
Cloning of Fruit-specific ACC Synthase and ACC Oxidase CDNAs
Papaya (Carica papaya L.) and Their Expression During Fruit
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Carica papaya ACC synthase mRNA, complete cds.
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/db_xref="taxon:3649"
/clone="pACSC2"
/tlssue_type="30% yellow fruit"
17. .1480
/note="fruit specific; ripening related"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 735; DB 8; Length 18
Pred. No. 1.1e-178;
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                                                                                                                             /product="ACC_synthase"
/protein_id="AAC98809.1"
/db_xref="G1:4090535"
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Best Local Similarity 70.8%;
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PHU88971 1757 bp mRNA linear PLN 22-SEP-1997 Pelargonium hortorum 1-aminocyclopropane-1-carboxylate synthase (GACS2) mRNA, complete cds.
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Bukaryota; Wagnoliophyta; eudicotyledons; core eudicots;
Rosidae; Geraniales; Geraniaceae; Pelargonium.
1 (bases I to 1757)
1 (Clark, D. G., Richards, C., Hilloti, Z., Lind-Iversen, S. and Brown, K. Effect of pollination on accumulation of ACC synthase and ACC oxidase transcripts, ethylene production and flower petal plant Mol. Biol. 34 (6), 855-865 (1997)
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Clark, D.G., Richards, C., Hilioti, Z., Lind-Iverson, S. and Brown, K.
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                                                                                                                                                                                                                                                                      DRETLVSLVSFINEKNIHLVCDEIYAATVFSQPAFVSIAEVIEQENVSCNRDLIHIVY
SLSKDMGFPCFRVGIVYSYNDAVVNCARKMSSFGLVSTQTQHLIASMLSDDEFVDTFI
VESARRLARRYTFFRGLAQVNIGCLKSNGGLFIWDLRRLLKEKTFFREMALWRVII
NEVKLNVSPGASFHCSEPGWFRVCFAMDDLTWQVALRRIITFALQNKEAAVLPAIKR
QCWQNNLGRLSLSFRDDFTWSPMSPHSPIQSPLVRAT"

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                                                                                                                                                               /note="similar to Pelargonium hortorum clone pGAC-2,
Genbank Accession Number U17231"
                                                                                                                  /note="1-aminocyclopropane-1-carboxylate synthase"
89. .1558
                                                                                                                                                                                                                                                                                                                                                                                                                                                            a State
PA 16802,
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Direct Submission
Submitted (07-FEB-1997) Horticulture, Pennsylvania
University, 102 Tyson Building, University Park, PA
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                               pollination'
                                                      hortorum"
                                                                                                                                                                                                                                                                                                                                                                       Query Match 37.4%; Score 719.2; DB 8; Best Local Similarity 70.9%; Pred. No. 1.3e-174; Matches 1000; Conservative 0; Mismatches 398;
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                                                                                                 ţ
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1. .1757
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ORIGIN
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L1868 bp DNA linear PAT 24-JUN-1998 CDNA encoding poplar ACC (1-aminocyclopropane-1-carbonic acid) synthetase which is induced by ozone.
E12806.1 GI:3251638
JP 1997075088-A/2.
unidentified.
unidentified.
unclassified.
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                                      atccatcaaatccattaggcacaatcatggacagaaagacactgagaaccgtggtgagct
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SOURCE
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9
                                                                                                                                                                                                                                                                        Length 1868;
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                                                                                                                                                      /clone='ppNA CCS2'
1. .118
119. .1579
/product-'Poplar ACC
(1-aminocyclopropane-1-carbonic synthetase which is induced by ozone' FT
.1868.
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                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                             'organism='Populus nigura
                                                                                                                                                                                                                                                                       36.0%; Score 691.6; DB 6;
llarity 71.7%; Pred. No. 1.8e-167;
Conservative 0; Mismatches 359;
                                                                                                                                                                                                                                                                                      0; Mismatches 359;
                                                                                                                       Location/Qualifiers
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Location/Qualifiers
1. 1868
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a 366 c 405 g 507
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                                                                                         strandedness: Double;
topology: Linear;
hypothetical: No;
                                                                                                                                                    /tissue_type='Leaf
                                                                                                                anti-sense: No;
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Matches 923;
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PLN 15-APR-2000
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
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                                                                                                                    tcataagcatagctgagatattagaggatgaaacagacatagagtgtgaccgcaacctcg
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Koch,J.R., Minocha,R., Nakajima,N., Yasutani,I., Saji,H.,
Rebbeck,J. and Davis,K.R.
Induction of ethylene and putrescine by ozone: Comparison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AB033503 1868 bp mRNA linear PLN Populus euramericana peacs-2 mRNA for l-aminocyclopropane-1-carboxylate synthase, complete cds
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AB033503.1 G1:7576443
1-aminocyclopropane-1-carboxylate synthase.
Populus euramericana (cultivar:I-45/51) cDNA to mRNA.
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Nakajima,N., Yasutani,I., Koch,J.R., Minocua,..., Tasutani,I., Koch,J.R., Minocua,..., Tasutani,I., Koch,J.R., Minocua,..., Tasutani,I., Tasutani,I.R. Rebbeck,J. and Davis,K.R.
Direct Submission
Submitted (12-OCT-1999) Nobuyoshi Nakajima, The National Institute
for Environmental Studies, Regional Environment Division; Onogawa
16-2, Tsukuba, Ibaraki 305-0053, Japan (E-mail:naka-320@nles.go.]p,
Tel:81-298-50-2490, Fax:81-298-50-2490)
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                           /LTAID 1 AL 100 -- "MERQHQLLSKIATNDRHGENSPYFDGWKAYDKNPFHPTDNPDGY
IQMGLAENQLSADSIIDMIKKHPKASICNPEGVHMFKDIANFODYHGLPEFRQAIAKF
MGRYRGGRYTPDPRIYWSGATMGANELIMFCLAPGPAFARDLGWRT
GVQIVPUDCDSSNNGDTIVAGLIAAYDKAQDGINYKGLITUPSPYTPAFYRDLGWRT
GVQIVPUDCDSSNNGDTIVAALTFSSQNFVSVSEVIEEVMDCNRDLIHIVYSLLSKDM
KLRGIFTKGLEQIGSTGKRKMSSFGLVSGOTOYLLASMLSDEEFVEDFLAESSKRL
KRHGIFTKGLEQIGISCLESRAGLEVWMNIRHLLKEQTNDGEMELMRVIVNDVKLNV
SPGSSFHTVEVERNMEDVETLEYALKRIHAFVGEQKREFILSTKTKDMPSKTR
CWKKNLRLSFSSRIFEEGIGSPLAMSPHSPLVRART"
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		5										
	Description	Mung bean 1-aminoc	Poplar 1-aminocycl	Pelargonium 1-amin	Papaya ACC synthas	Tomato 1-aminocycl	Tomato ACC synthas	Coffee-fruit speci	Tomato ACC synthas	Poplar 1-aminocycl	Tomato 1-aminocycl	Tomato ACC synthas
	ID	AAY79292	AAW21754	AAW60235	AAW57484	AAE00986	AAB59724	AAW52818	AAR15509	AAW21755	AAE00985	AAB59723
	DB	21	18	19	19	22	22	19	12	18	22	22
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ALIGNMENTS

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RESULT

Mung bean; 1-aminocyclopropane-1-carboxylic acid synthase; ACC synthase; AIM-1; promoter; pGEL-1; transgenic plant. Mung bean 1-aminocyclopropane-1-carboxylic acid synthase. AAY79292 standard; Protein; 484 AA. Botella Mesa JR, Cazzonelli CI; 99WO-AU00705. 98AU-0005572. 03-JUL-2000 (first entry) (UYQU) UNIV QUEENSLAND. WPI; 2000-270821/23. N-PSDB; AAZ94267. WO200012714-A1. Vigna radiata 31-AUG-1999; 31-AUG-1998; 09-MAR-2000. AAY79292; AAY79292

Isolated nucleic acid molecule for producing transgenic plants having altered characteristics such as resistance to a plant pathogen comprises promoter, inducible in response to physical stimulation -

95JP-0254510 95JP-0254510

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Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic enzyme genes - from poplar tree, are useful for generating ozone-resistant trees and pollution clean-up trees
                                                                                                                                                                                                               Claim 2; Pages 7-9; 12pp; Japanese.
                                                                                                             (TOYT ) TOYOTA JIDOSHA KK.
                                                                                                                                   WPI; 1997-239270/22.
                                                                                                                                               N-PSDB; AAT73501
  Poplar nigra.
                       JP09075088-A.
                                                                  07-SEP-1995;
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                                             25-MAR-1997.
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                 The present sequence is that of 1-aminocyclopropane-1-carboxylic acid synthase (ACC synthase) of mung bean. ACC synthase expression is induced in response to mechanical strain, auxin and salt stress. The invention relates to the promoter, pGEL-1 (see AAZ94266), of the ACC synthase gene, AIM-1. pGEL-1 is capable of induction by the induction by hysical and/or environmental stimuli in cells in which it is indigenous and, in the absence of any negative regulatory mechanism, is capable of constitutive expression in cells in which it is non-indigenous. The promoter can be used to direct expression of sense conferring useful traits on plants, such as improved resistance to a plant pathogen, altered nutritional characteristics, expression of a plantabody, altered blochemical pathway, altered flower colour.
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; Pred. No. 1.6e-247;
0; Mismatches 0; I
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Claim 41v; Page 101-103; 111pp; English.
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This protein is a 1-aminocyclopropane-1-carboxylic acid (ACC) synthase encoded by a cDNA clone isolated from poplar trees which had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone for 6 hours after one hour accilmation at 25 degrees C, 70 % relative humidity, 30 k lux and air current 30 cm/second. The gene will be useful for breeding air pollutant ozone-resistant trees, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 VSTQTQYQLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQ-SNAGLFVWM 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMDDMAVQIALO 429
                                                                                                                                                                                                                                                                                                                                                                                                                                        PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSGGATG 130
                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                           89
                                                                                                                                                                                                                                                                                                                                             11 LLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDWILNN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVFSQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMSSFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              430 RIRNEVLQNKEVVVSNKKHCWHSNLRLSLKTRRFDDITMSPHSPLPQSPMVKATN 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 481;
                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                        DB 18;
                                                                                                                                                                                                                                                     73.5%; Score 1881.5; DB 18
73.5%; Pred. No. 1.3e-179;
ive 58; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
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                                                                                                                                                                                                                                                     Query Match 73.5
Best Local Similarity 73.5
Matches 349; Conservative
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                                                                                                                                                                                  481
                                                                                                                                                                                       Sequence
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AAW57484;
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9
                                                                                                                                                                                                                                                                                                                                                               synthase (ACC synthase) of geranium cv. Sincerity was deduced from isolated CDNA clone pHSacc49 (see AAV30326). This ACC synthase has a mol.wt. of 55.1 kpa and is dealgnated as a Group II enzyme, 2 Group I geranium ACC synthases (see AAV80233 and AAW80234) are also claimed. The invention relates to new isolated ACC synthase genes from geranium and rose (see AAV80324.25 and AAV3030) and the use of antisense fragments of these genes to control expression of ACC synthase genes in transgenic plants, especially in geranium, rose and woody plants. By reducing the amount of ACC synthase produced in plant cells, the rate of ACC conversion to ethylene can be decreased. This can be used to prolong the shelf-life of cut flowers and to reduce leaf yellowing and petal abscission during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGAHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVP-VMCDSSNNFVLTKEA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 FSQPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKM 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 DQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDW 66
                                                                                                                                                                                                                                                                                                                                                         This amino acid sequence of this 1-aminocyclopropane-1-carboxylate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATV
                                                                                                                                                                                                                                                                                      New isolated ACC synthase genes - are obtained from geranium and rose, used to develop products for producing plants with reduced ethylene levels, for increasing shelf-life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19; Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59; Indels
                                                                ACC synthase; 1-aminocyclopropane-1-carboxylate synthase; ethylene; transgenic plant; wilting; geranium; pPHSacc49.
                                           Pelargonium 1-aminocyclopropane-1-carboxylase synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.3%; Score 1875.5; DB 1
71.9%; Pred. No. 5.3e-179;
ive 68; Mismatches 59;
                                                                                                                                                                                                           (COLS ) UNIV COLORADO STATE RES FOUND.
                                                                                                 Pelargonium x hortorum cv. Sincerity.
                                                                                                                                                                                                                                                                                                                                   Claim 58; Fig 8; 77pp; English.
                                                                                                                                                                 97WO-US17644
                                                                                                                                                                                      96US-0724194
                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 71.9
Matches 348; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     shipping and storage
                                                                                                                                                                                                                                                       WPI; 1998-260994/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 490 AA;
                                                                                                                                                                                                                                                                   N-PSDB; AAV30326.
                     28-SEP-1998
                                                                                                                      709814465-A1
                                                                                                                                                                30-SEP-1997;
                                                                                                                                                                                      01-OCT-1996;
AAW60235;
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                                                                                                                                                                                                                                 Ranu RS;
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This is a papaya 1-aminocyclopropane-1-carboxylic acid synthase (ACC synthase). The encoding nucleotide sequences are useful for the recombinant production and control of ACC synthase in transformed plants and cells, especially to control fruit ripening. The enzyme converts responsible for the ripening of fruit (ACC is converted to ethylene by CC oxidase). Commercial tropical fruit markets e.g. papaya production, require fruits in an adequately ripened state. Ripening is dependant on various conditions such as temperature and time. By providing ACC synthase conditions such as temperature and time. By providing ACC synthase conditions, the endogenous enzyme can be inhibited using antisense constructs, until it reaches its destination, then allowed to ripen, or be used in recombinant cells which can produce ethylene and in cripen fruit. Control or inhibition of ethylene production with nucleic acids is safer than chemical means, which can be toxic, and cannot be used for commercial inhibition.
                                                                                                                                                                                                                                                                               IALORIRNEVICONKEVVV -- SNKKHCWHSNL-RLSLKTRRFDDIT---MSPHSPLPQSPM 479
SSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGL 365
                                 FVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMDDMAVQ 425
                                                                                                                                                                                  Papaya; ACC synthase; ethylene biosynthesis; fruit ripening; enzyme; 1-aminocyclopropane-1-carboxylic acid synthase; regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Papaya ACC synthase cDNA sequence – useful for regulating ethylene blosynthesis in the ripening of fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Columns 35-40; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW57484 standard; Protein; 487 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-0485107.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Papaya ACC synthase enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-AUG-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neupane KR, Stiles JI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYHA-) UNIV HAWAII.
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N-PSDB; AAV31482.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480 VKAT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-JUN-1995;
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DB 19; Length 487;

71.2%; Score 1823;

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Gaps 70 72

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synthase, LE-ACC 1B. ACC synthase are capable of catalysing the conversion of AdoMct (S-adenosyl methionine) to ACC and methyl thioadenosine (MTA). ACC DNA is useful for producing ACC synthase which is essential for the production of ethylene in higher plants, where ethylene is a determinant of fruit ripening. The ACC DNA is also useful for producing transgenic plants which are overproducers of or are deficient in ACC synthase.
                                                                                                                                                                                                                                                                                                71 PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSGGATG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC sylchase; 1-aminocyclopropane-1-carboxylic acid synthase; enzyme; ethylene production; fruit ripening; tomato; LE-ACC.
                                                                                                                                                                                                                                                        AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY
                                                                                                                                                                                                                                                                                                                                                                         EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVFSQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                     371 LRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMDDMAVQIALOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDWILNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMSSFGL
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                                                                                                                                                                                  Length 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            431 IRNFVLQNKEV -- VVSNKKHCWHSNLRLSLKTRRFDDITMSPHSPLPQSPMVK
                                                                                                                                                                             Query Match 69.2%; Score 1771.5; DB 2
Best Local Similarity 68.9%; Pred. No. 1.4e-168;
Matches 326; Conservative 76; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACC synthase gene LE-ACC1B(b) clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
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92US-0862493.
95US-0481171.
90US-0579896.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB59724 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0033349
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                                                                                                                                   483 AA;
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02-APR-1992;
07-JUN-1995;
10-SEP-1990;
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                                                                                                                                      Sequence
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                             3,
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                                                                                                                                EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVFSQPG 250
                                                                                                                                                                                                                                                                    249
                                                                                                                                                                                                                                                                                             FISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMSSFGL 310
                                                                                                                                                                                                                                                                                                                            308
                                                                                                                                                                                                                                                                                                                                                      VSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD 370
                                                                                                                                                                                                                                                                                                                                                                       430
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                         70
                                                                        present sequence is tomato 1-aminocyclopropane-1-carboxylic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431 IRNFVLQNKEVVVSNKKHCWHSNLRLSLKTRRFDDIT-----MSPHSPLPQSPMVKA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDWILNN
                                                                                                                  PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSGGATG
                                                                                                                                                                             AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY
                                                                                                                                                                                                                                                                                                                                                                                                               LRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMDDMAVQIALQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tomato, 1-aminocyclopropane-1-carboxylic acid synthase; LE-ACC 1B; ethylene production; fruit ripening; transgenic plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tomato 1-aninocyclopropane-1-carboxylic acid synthase, LE-ACC 1B.
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8
                             Indels
            9.7e-174;
          Pred. No. 9.75
5; Mismatches
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                             65;
          70.9%;
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90US-0579896
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                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OF AGRIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lycopersicon esculentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-289591/30.
            Best Local Similarity
Matches 339; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (USDA ) US SEC
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10-SEP-1990;
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AAE0098 XXX XXX AAC AA XXX XXX XXX TC XXX TC XXX CT XXX CT XXX CT

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synthase;

97WO-US14184. 96US-0695412.

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Coffee-fruit; 1-aminocyclopropane-1-carboxylic acid ACC synthase; ethylene biosynthesis; fruit ripening.
           Coffee-fruit specific ACC synthase,
                                                                                                                                                                                          (UYHA-) UNIV HAWAII.
                                                                                             WO9806852-A1
                                                                                                                                            11-AUG-1997;
                                                                                                                                                                  12-AUG-1996;
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                                                                                                                                                                                                                                                                                                                                                                         3,
                                                                                                                                                            1-aminocyclopropane-1-carboxylic acid (ACC) synthase is essential for the production of ethylene in higher plants; ethylene is a determinant of fruit ripening. The present invention relates to an expression cassette which comprises the reverse transcript of RNA complementary to an RNA transcribed from ACC synthase gene. The expression cassette can be seed to prevent ACC gene expression. The expression cassette can be for inhibiting ethylene production and fruit ripening, when introduced into a plant or plant cells. The present sequence is the protein encoded by tomato ACC synthase gene LE-ACCIB(b) clone. This sequence was used in a sequence homology comparison with other ACC synthase gene clones
                                                                               Expression cassette for producing transgenic plants exhibiting inhibited ethylane production and delayed fruit ripening, comprises complementary RNA which inhibits 1-aminocyclopropane-1-carboxylic acid synthase synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 ahemlafcladpgdaflyptpyypgfdrdlrwrtgyqlfpyycescndfkyttkaleeay 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY 190
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                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 483;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    431 IRNFVLQNKEV -- VVSNKKHCWHSNLRLSLKTRRFDDITMSPHSPLPQSPMVK 481
                                                                                                                                                                                                                                                                                                                                                                        66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.2%; Score 1771.5; DB 2
68.9%; Pred. No. 1.4e-168;
ive 76; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW52818
ID AAW52818 standard; Protein; 504 AA.
                                                                                                                                         Example 3; Fig 10; 91pp; English
           (USDA ) US DEPT OF AGRICULTURE.
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                                                                                                                                                                                                                                                                                                                                                           Local Similarity ve.. nes 326; Conservative
                                 Theologis A;
                                                      WPI; 2001-079558/09
                                                                                                                                                                                                                                                                                                             483 AA;
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                                 Sato T,
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1-mainocyclopropane-1-carboxylic angular, control ethylene blosynthesis in coffee plants, as AcC synthase is an element of the ethylene coffee plants as AcC synthase is an element of the ethylene blosynthesis in blosynthesis pathway. Transformation of wild-type coffee plants with constructs containing the cDNA in an antisense orientation can block AcC synthase synthesis. The cDNA can also be used to block AcC synthase synthesis by co-suppression. Plants transformed with the cDNA are incapable of synthesising ethylene, which is necessary in the final stages of fruit ripening in coffee, therefore ethylene application enables fruit ripening to be controlled, e.g. application to the entire plant can synchronise ripening. Coffee beans are preferably obtained from mature fruit, but non-uniform ripening has necessitated laborious hand-picking, or low yields and productivity when harvesting by strip harvesting or mechanical techniques. The ability to synchronise ripening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 ILNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATGAHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEAL 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 DQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDW 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACC synthase and ACC oxidase from coffee, Coffee arabica - and encoding DNA, useful in methods to control coffee bean ripening e.g. to allow synchronous ripening and thus more productive harvesting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
                                                                                                                                                                                                                                                                                                                                                            The present sequence is Coffea arabica, coffee-fruit specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 504;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1765; DB 19;
Pred. No. 6.6e-168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nakes mechanical harvesting more productive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83; Mismatches
Stiles JI;
                                                                                                                                                                                                                                                                                            Claim 1; Fig 1; 72pp; English.
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Moisyadi I, Neupane KR,
                                                            WPI; 1998-159543/14.
N-PSDB; AAV20947.
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Best Local
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72

13 llskiatndghgenspyfdcwkayannpfhltdnptgviqmglaenqlcfdliqewmvnn

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us-09-763-957-2.rag

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(Note: Revised entry submitted to correct the patent number format of US Government-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic clone LE-ACCIA was one of four different clones identified in a library prepared from total DNA extracted from etiolated Rutgers seedlings. Screening was by the cDNA clone ptACCI (see AAQ15134). The amino acid sequence was deduced from the cDNA and shows constderable homology with ACC sequences deduced from the tromato and the zucchini clones.
              426
                                                                                425
                                                                                                        427 ALQRIRNFVL-QNKEV-VVSNKKHCWHSNLRLSLKTRRFDDIT-----MSPHSPLPQ--- 476
                                                                                                                          367 VWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMDDMAVQI
                                                                   SFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding ACC synthase - used for control of plant development for prodn. of ACC synthase, ethylene and ethanol
                                                                                                                                                                                                                                                                                                                                                                              1-aminocyclopropane-1-carboxylic acid synthase; fruit ripening
                                                                                                                                                                                                                                                                                                                                                     Tomato ACC synthase encoded by clone LE-ACC1B
                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum c.v. Rutgers.
                                                                                                                                                                                                                                                        AAR15509 standard; Protein; 483 AA.
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                                                                                                                                                              ---SPMVKAT 483
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486 gshmmsphspmasplvrat 504
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(first entry)
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09-MAR-1992
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This protein is a 1-aminocyclopropane-1-carboxylic acid (ACC) synthase encoded by a cDNA clone isolated from poplar trees which had been exposed to ozone. Exposure conditions were: 0.1 ppm ozone for 6 hours after one hour acclimation at 25 degrees C, 70 % relative humidity, 30 k lux and air current 30 cm/second. The gene will be useful for breeding air pollutant ozone-resistant trees, especially poplar.
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             EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVFSQPG
                                                                                                                  FISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMSSFGL
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                                                  AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY
                                                                                                                                                                                                       VSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ozone-induced 1-amino:cyclopropane-1-carboxylic acid synthetic enzyme genes - from poplar tree, are useful for generating ozone-resistant trees and pollution clean-up trees
                                                                                                                                                                                                                                                                                                         431 IRNFVLQNKEV--VVSNKKHCWHSNLRLSLKTRRFDDITMSPHSPLPQSPMVK 481
                                                                                                                                                                                                                                                                                                                        Ozone; induction; exposure; resistance; transgenic plant; ACC; 1-aminocyclopropane-1-carboxylic acid biosynthesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pollar 1-aminocyclopropane-1-carboxylic acid synthase PNACCS2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2; Pages 9-11; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                AAW21755 standard; Protein; 486 AA
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DB 12; Lengt 167; 67; Indels

68.9%; Score 1762.5; DB ... 68.7%; Pred. No. 1.1e-167. ... Mismatches 67

Matches 325; Conservative

11

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Similarity

Local

Length 483;

LLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDWILNN 70

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Lycopersicon
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Matches 327;
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                                                                                                         Sequence
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                                                                                                         247
                                                                                                                                                                                                      307
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|krihafvgeqkeret1stktkdmpsktkcwkkn1r1sfssrifeegigspiamsphsp1 481
                                                                                              LNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFWARTRGNRITFDPDRIVMSGG 127
                                                                                                                                 ATCAHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALE 187
                                                                                                                                                                                                                                        FGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFV 367
                                                                                                                                                                                                                                                                          WMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMDDMAVQIA 427
                                                                                                                                                                                                                                                                                                            LQRIRNFV-----LQNKEVVVSNKKHCWHSNLRLSLKTRRFDD-----ITMSPHSPL 474
                                             Gaps
                                                            QTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDWI 67
                                                                      Tomato, 1½aminocyclopropane-1-carboxylic acid synthase; LE-ACC 1A;
ethylene production; fruit ripening; transgenic plant.
                                                                                                                                                                   DAYERAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVFS
                                                                                                                                                                            QPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMSS
                           486;
                                           15;
                          DB 18; Length
                                           72; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           aminocyclopropane-1-carboxylic acid synthase,
                                   Pred. No. 1:1e-167
68; Mismatches 72
                         68.9%; Score 1762.5;
67.7%; Pred. No. 1:1e
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90US-0579896.
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                         Query Match 68.9°
Best Local Similarity 67.7°
Matches 325; Conservative
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486
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                                           The present sequence is tomato 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC 1A. ACC synthase are capable of catalysing the conversion of AdoMet (S-adenosyl methionine) to ACC and methyl thioadenosine (MTA). ACC DNA is useful for producing ACC synthase which is essential for the production of ethylene in higher plants, where farthylene is a determinant of fruit ripening. The ACC DNA is also useful for producing transgenic plants which are overproducers of or are deflicient in ACC synthase.
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                                                                                                                                                                                                                                                                                                                                         Length 485;
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                                                                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                                                                                                                                                         65;
                                                                                                                                                                                                                                                                                                                                      68.6%; Score 1755.5; DB 22
68.8%; Pred. No. 5.6e-167;
ive 76; Mismatches 65;
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Example 3; Fig 10; 92pp; English.
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27; Conservative
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first entry)

(updated)

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1-aminocyclopropane-1-carboxylic acid synthase; fruit ripening
                                                               Tomato ACC synthase encoded by clone LE-ACCIA
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                                  17-DEC-2001
                                            09-MAR-1992
            AAR15508
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                                                                                                                                                                                            1-aminocyclopropane-1-carboxylic acid (ACC) synthase is essential for the production of ethylene in higher plants; ethylene is a determinant of frult ripening. The present invention relates to an expression cassette which comprises the reverse transcript of RNA complementary to an RNA transcribed from ACC synthase gene. The expression cassette can be used to prevent ACC gene expression. The expression cassette is useful for inhibiting ethylene production and frult ripening, when introduced into a plant or plant cells. The present sequence is the protein encoded by tomato ACC synthase gene LE-ACCIA(b) clone. This sequence was used in a sequence homology comparison with other ACC synthase gene clones
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                                                                                                                                                                                                                                                                                                                                                                                                                              72
                                                                                                                     Expression cassette for producing transgenic plants exhibiting inhibited ethylene production and delayed fruit ripening, comprises complementary RNA which inhibits 1-aminocyclopropane-1-carboxylic ac
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                                                                                                                                                                                                                                                                                                                                                                                     76; Mismatches
                                                                                                                                                                           Example 3; Fig 10; 91pp; English,
                                                     (USDA ) US DEPT OF AGRICULTURE
95US-0378313.
92US-0862493.
95US-0481171.
90US-0579896.
                                                                                                                                                                                                                                                                                                                                                                                     327; Conservative
                                                                           Theologis A;
                                                                                                 WPI; 2001-079558/09
                                                                                                                                                      synthase synthesis
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                                                                                                                                                                                                                                                                                                                                485 AA;
                                                                                                                                                                                                                                                                                                a sequence homolog
(AAB59721-B59727).
25-JAN-1995;
02-APR-1992;
07-JUN-1995;
                               10-SEP-1990;
                                                                                                                                                                                                                                                                                                                                Sequence
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(Note: Revised entry submitted to correct the patent number format of Sovernment-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/dwpi/updates/ntis_us.html.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      in a library prepared from total DNA extracted from etiolated Rutgers seedlings. Screening was by the CDNA clone prACCI (see AAQ15134). The amino acid sequence was deduced from the CDNA and shows considerable homology with ACC sequences deduced from the three other
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomic clone LE-ACC1A was one of four different clones identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           encoding ACC synthase - used for control of plant development for prodn. of ACC synthase, ethylene and ethanol
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68.6%; Pred. No. 4.5e-166;
:1ve 76; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 14; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tomato and the zucchini clones.
See AAQ15131-Q15140.
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                                                                                         900S-0579896
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Best Local Similarity 68.69
Matches 326; Conservative
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USN7579896-N.
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                                                                                         10-SEP-1990;
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AAR15508 standard; Protein; 485

RESULT 12

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01-JUN-1998
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25-JAN-1995;
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(Note: Revised entry submitted to correct the patent number format of SGovernment-owned NTIS applications to prevent clashes with ongoing US granted patent numbers. For further information please visit the Derwent web site at www.derwent.com/derwelt.library.html.)
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                    61 DLVEDWILNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encoding ACC synthase - used for control of plant development for prodn. of ACC synthase, ethylene and ethanol
                                                                                                                 484
                                                                            431 IRNFVLQNKEV--VVSNKKHCWHSNLRLSLKTRRFD-DITMSP-HSPLPQSPMVK 481
                                                                                                                                                                                                                                                                                                                                                                                                yclopropane-1-carboxylic acid synthase; fruit ripening.
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; Pred. No. 1e-162;
72; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                         ACC synthase encoded by clone LE-ACC2.
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                                                                                                                                                                                               AAR15507
ID AARU5507 standard; Protein; 485 AA.
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09-MAR-1992
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301 CARKMSSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQ 360
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1-aminocyclopropane-1-carboxylic acid (ACC) synthase LE-ACC2.

1-aminocyclopropane-1-carboxylic acid (ACC) synthase LE-ACC2.

1-E-ACC2 was used in the isolation of conserved sequences from five tomato (LE-ACC 1A, LE-ACC 1B, LE-ACC3, LE-ACC3 and LE-ACC4) and two zucchini (CP-ACC 1A and CP-ACC 1B) ACC synthases.

A novel DNA molecule comprises an expression system which, when contained in a plant host cell, generates RNA that is sufficiently complementary to an RNA transcript of an endogenous ACC synthase gene to prevent its synthesis. The expression system consists of the reverse transcript of the antisense RNA (i.e. CDNA) operably
                                                                                                                             YAATVFSQPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVN
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950S-0378313.
95US-0481171.
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                                                                                                                        MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTS 60
linked to control sequences that effect its transcription into the antlsense RNA, where the CDNA can be amplified from the endogenous ACC synthase gene by primer pairs encoding conserved ACC synthase sequences. The DNA molecule can be used to delay ripening of tomato or zucchini fruits.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Encoded by GTT; this translation exception
Appurs while decoding LE-ACC2 cDNA (AAD04546)"
                                                                                                                                                                                                                                                           CARKMSSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQ
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                                                                                              Indels
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                                                                      Score 1713; DB 19;
Pred. No. 1e-162;
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The present sequence is tomato 1-aminocyclopropane-1-carboxylic acid synthase, present sequence is tomato 1-aminocyclopropane-1-carboxylic acid synthase, product of AdoMet (S-adenosyl methionine) to ACC and methyl thioadenosine (MTA). ACC DNA is useful for productine ACC synthase which is essential for the production of ethylene in higher plants, where ethylene is a determinant of fruit ripening. The ACC DNA is also useful for producing transgenic plants which are overproducers of or are deficient in ACC synthase.
                                                                                                                                                                                                                                                       Novel isolated DNA molecule encoding 1-aminocyclopropane-1-carboxylic acid synthase, LE-ACC2 useful for producing ACC synthase which is essential for the production of ethylene in higher plants -
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Pred. No. 1e-162;
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Best Local Similarity 65.6%; Pr
Matches 319; Conservative 72;
                                                                                                                                                                                                                                                                                                                                                 Claim 1; Fig 5; 92pp; English,
95US-0378313
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90US-0579896
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psplvr
25-JAN-1995;
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10-SEP-1990;
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	Copyright

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US-09-763-957-2 2559 1 MGFKAMDQTPLLSKWAIGDG.........DITMSPHSPLPQSPMVKATN 484

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues Searched:

Total number of hits satisfying chosen parameters:

105224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	P31531 qlycine max						-	cucurbita	P27486 dianthus ca			P37821 malus domes	Q00257 cucurbita m		aguifex		Q60013 streptomyce		P53001 bacillus su	Q58097 methanococc	Q59228 bacillus st	Q9x0y2 thermotoga		Q9v0l2 pyrococcus	P58350 rhizobium m	033822 thermus agu	P33447 trypanosoma		P39643 bacillus su	P34106 panicum mil	P52894 hordeum vul	Q56232 thermus agu	267 mycobact
SUMMARIES	ar ar	1A1C_SOYBN	1A1C_PHAAU	1A1C_TOBAC	1A12_LYCES	1A11_PRUMU	1A11_CUCMA	1A11_CUCPE	1A12_CUCPE	1A1C_DIACA	1A14_LYCES	1A12_ARATH	1A1C_MALDO	1A12_CUCMA	1A11_ORYSA	AAT_AQUAE	AAT_BACSP	AAT_STRVG	PATA_BACSU	AAT1_BACSU	AAT2_METJA	AAT_BACST	AAT_THEMA	AAT_RICPR	AAT_PYRAB	AAB1_RHIME	AAT_THEAQ	ATTY_TRYCR	AAB2_RHIME	AAT2_BACSU	ALA2_PANMI	ALA2_HORVU	AAT_THETH	AAT_MYCTU
	DB	7	7	-	-	Н	Н		Н	-	-	-		Н	-	-	-	-	-	-	-	-	-	Η.	-	٦.	-	Н	Н	П	7	ч	-	
	Length	484	368	491	485	492	493	493	464	517	476	496	473	475	487	394	392	397	392	393	370	393	377	412	386	410	383	416	410	399	482	482	382	429
% Query		92.0	75.3	68.0	6.99	66.4	4	64.0	63.6	62.7	61.9	7	52.4	52.3	49.2	11.5	10.8	10.7	٠	٠	œ.	9.7			٠	•		8.8		٠		8.5	•	
	Score	2354	1927	1739.5	. 1713	1698.5	1640.5	1637.5	1627.5	1603.5	1584	1578	1341	1339.5	1258.5	293,5	276.5	274.5	263	256.5		248.5	248	229	227	225.5	225	224	222.5	220.5	220	217.5	217	216.5
Result	No.	1	7	m	4	Ω.	9	7	ω .	o ·	10	11	12	13	14	15	16	17	18	19	20	21	22	23	54	25	26	27	28	29	30	31	32	33

P52892 saccharomyc P04694 rattus norv P77434 escherichia P24298 homo sapien P77727 escherichia P71348 hemophilus P1735 homo sapien Q10334 schlzosacch P52893 saccharomyc O58489 pyrococcus Q55128 synechocyst Q60317 methanococc		a. (e) (EC 4.4.1.14) (ACC (ACC 1)	Embryophyta; Tracheophyta; dons; core eudicots; Rosidae; ideae; Phaseoleae; Glycine.	nk/DDBJ databases. OF 1-AMINOCYCLOPROPANE-1- OF THYLENE IN HIGHER PLANTS. Hethlonine = 1- methylthloadenosine. STEP OF ETHYLENE BIOSYNTHESIS. PYRIDOXAL-PHOSPHATE-DEPENDENT	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	Lyase; Pyridoxal phosphate; PHOSPHATE (BY SIMILARITY). 28992987 CRC64;	DB 1; Length 484; 5e-174; ies 23; Indels 0; Gaps 0;
507 1 ALAT_YEAST 454 1 ATT_RAT 412 1 YFDZ_ECOLI 495 1 ALAT_HUMAN 405 1 YFBQ_ECOLI 404 1 YFBQ_ECOLI 404 1 YFBQ_RAEIN 454 1 ATTY_HUMAN 505 1 ALAM_YEMST 391 1 AAT_EXPRO 389 1 AAT_SYNY3 375 1 AATL_METJA	ALIGNMENTS	STANDARD: PRT; 484 AA. 1. 26, Created) 1. 26, Last sequence update) 1. 37, Last annotation update) 10 37, Larbaylate synthase (EC 4.4.1.14) (ACC enosyl-L-methionine methylthioadenosine-lvase)	ACS1. dilyciam (Soybean). Eukaryota: Viridiplantae; Streptophyta; Embryol Spermatophyta; Magnoliophyta; eudicotyledons; derosidas I; Fabales; Fabaceae; Papilionoideae;	WE-Leaf; Lhe EMBL/GenBa THE FORMATION THE FORMATION S-adenosyl-L-T Carboxylate + PHOSPHATE. RATE LIMITING	This SWISS-PROT entry is copyright. It is pertween the Swiss Institute of Bioinformat the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (see or send an email to license@ilsb-sib.ch).	EMBL, X67100; CAA4744.1; PIR; S25002; S25002. PIR; S25002; S25002. INSEPP. P37821; IBG. InterPro; IPR001176; ACC_Synthase. InterPro; IPR001176; ACC_Synthase. InterPro; IPR001151; Aminotran_1. Pfan; PF00155; aminotran_1.2: 1. PRINTS; PR00753; ACCSYNTHASE. PROSTIE; PS001056; AA_TRANSFER_CIASS_1; 1. Fruit ripening; Ethylene biosynthesis; Lyase; Py; Multigene family. BINDING .279 279 PYRIDOXAL PHOSPHATE SEQUENCE 484 AA; 54730 MW; I52F7AD12B992987 (0%; Score 2354; 9%; Pred. No. 4 21; Mismatch
216.5 8.5 213.5 8.3 202.5 7.9 201.5 7.9 196.5 7.7 194.5 7.6 194.5 7.6 194.5 7.6 189.5 7.4		1 OYBN 31531, 31531, 1-IIII-1993 (Re 1-UUL-1993 (Re 5-DEC-1998 (Re -aminocycloproy	CS1. 'lycine max (Soybea lukaryota, Viridipl. permatophyta; Magn urosids 1; Fabales CBI_TAXID=3847;	NCHL TAXID=384/; (1) SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRANH-CY. CENTURY; TISS SATA. D. Li N. MALTOO A. Submitted (JUN-1992) to[- FUNCTION: CATALYZES TARDOXYLATE, A DIREC CATALYTIC ACTIVITY: aminocyclopropane-1 COFACTOR: PYINDOXAL PATHWAY: FIRST, AND SUBUNIT: HOMODIMER SIMILARITY: BELONGS	This SWISS-PROT entractions of the European Bioinfo use by non-profit modified and this stenties requires a or send an email to	EMBL; X67100; CAA4744.1; PIR; S55002; S25002. HSSP; P37821; IBSG. Mendel; 8361; GLYma; Acs;1. InterPro; IPRO01176; ACC_Synthase InterPro; IPRO01176; ACC_Synthase InterPro; PR001175; aminotran_1.2; PRNINTS; PR00753; ACCSYNTHASE. PROSTEE; PS00105; AA_TRANSFER CLA, Fruit ripening; Ethylene blosynth Multigene family. BINDING 279 PYRII SEQUENCE 484 AA; 54730 MW; 15	y Match Local Similarity 90. hes 439; Conservative
		32 1		2			Query M Best Lo Matches

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A Phillips A.T.; Arteca J.M., Schlagnhaufer C.D., Arteca R.N.,
A Phillips A.T.; Arteca J.M., Schlagnhaufer C.D., Arteca R.N.,
Tadentification and characterization of a full-length cDNA encoding
for an auxin-induced 1-anthocyclopropane-1-carboxylate synthase from
etiolated mung bean hypocotyl segments and expression of its mRNA in
response to indole-3-acetic acid.";
Plant Mol. Biol. 20:425-436(1992).
C.-I. PONCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
C.-I. CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-
aminocyclopropane-1-carboxylate + methylthioadenosine.
C.-I. CATALYTIC ACTIVITY: S-ADENOXILE + methylthioadenosine.
C.-I. PATHWAY: ETSET, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
C.-I. SUBUNIT: HOMODIMER.
C.-I. INDUCTION: HORMONES, SUCH AS AUXIN, ENVIRONMENTAL FACTORS, SUCH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDUCTION: HORMONES, SUCH AS AUXIN, ENVIRONMENTAL FACTORS, SUCH AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phaseolus aureus (Mung bean) (Vigna radiata).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyladons; core eudicots; Rosidae;
Surosida I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
                                                                                                                                                                                                                                                                       CARKMSSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQ 360
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                                                                            RIVMSGGATGAHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFV 180
                                                                                                                              LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEI 240
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                          SNAGLEVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMD
            MGFKAMDQTPLLSKWAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMOMGLAENQLTS
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01-UUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
1-DEC-1998 (Rel. 37, Last annotation spathase (EC 4.4.1.14) (ACC synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-CV. BERKEN / RWILCZ; TISSUE-Hypocotyl;
MEDLINE-93043033; PubMed-1421146;
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Q01912;
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MECHANICAL WOUNDING AND A NUMBER OF CHEMICALS.
SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                            Mendel; 9876; PHAau; Acs; 5.
InterPro; IPR01511; Aminotran_1.
InterPro0155; aminotran_1.2; 1.
PROSITE; PS00105; AA_TRANSFER.CLASS_1; 1.
FRUIT ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
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01-0CT-1994 (Rel. 30, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
11-aninocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (ACC synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 368
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Pred. No. 2.6e-141;
1; Mismatches 0;
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Best Local Similarity 99.7%;
Matches 367; Conservative 1
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368
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SEQUENCE
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Bailey B.A., Avni A., Li N., Matoo A.K., Anderson J.D.;
"Nucleotide sequence of the Nicotiana tabacum cv Xanthi gene encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DLVEDWILNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGFKAMDQTPLLSKWAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVWQMGLAENQLTS 60
                                                                                                                                                                                                                                                                          COFACTOR: PYRIDOXAL PHOSPHATE.
PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
SUBBNIT: HOMODIMER.
SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P37821; IBBG.

Mendel; 222; NICLA; ACC_synthase.
InterPro; IPR001176; ACC_synthase.
InterPro; IPR001511; Aminotran_1_2; 1.
Pfam; PF00155; aminotran_1_2; 1.
PRINTS; PR00753; ACCSYNTHASE.
PROSITE; PS001055; AA_TRANSFE.
Fruit Tipening; Ethylene blosynthesis; Lyase; Pyridoxal phosphate.
BINDING 278 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNAGLFVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMD
                                                                                                                                 1-aminocyclopropane-1-carboxylate synthase.";
Plant Physiol. 100:1615-1616(1992).
-!- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-CARBOXYLATE, A DIRECT PRECURSON OF ETHYLENE IN HIGHER PLANTS.
-!- CATALYTIC ACTIVITY: S-adenosyl.L.methionine = 1-aminocyclopropane-1-carboxylate + methylthioadenosine.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.0%; Score 1739.5; 66.5%; Pred. No. 1.1e
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Sukaryota, Viridiplantae; StreptCopyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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TISSUE-Etiolated hypocotyl;

MEDLINE-92106351; PubMed=1762159;

NCTMANN W.H., Peter G.F., Oeller P.W., Keller J.A., Shen N.F.,

Nagy B.P., Taylor L.P., Campbla A.D., Theologis A.;

"1-aminocyclopropane-1-carboxylate synthase in tomato is encoded in the second and second a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1994 (Rel. 30, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1-aminocyclopropara -1-carboxylate synthase 2 (EC 4.4.1.14) (ACC synthase 2) (S-adenosyl-L-methionine methylthioadenosine-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    485 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-CV. ORLANDO; TISSUE-Fruit; MEDLINE-90280476; Pubmed~2191304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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InterPro; IPR00151; Aminotran_1.
Pfam; PF00155; aminotran_1_2; 1.
PRINTS; PR00753; ACCSYNTHASE.
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J. Mol. Biol. 222:937-961(1991).
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EMBL; X59145; CAA41856.1; -.
EMBL; M34289; AAA81580.1; -.
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PIR; S19678; S19678.
PIR; A35516; A35516.
HSSP; P37821; 1B8G.
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480 PIPHSPLVRA 489
                                                                                                473 PLPQSPMVKA 482
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192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Prunus mume (Japanese flowering apricot).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Rosaceae; Prunus.
                                                                                                                     Gaps
                                                                                                                                               1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTS 60
       AA_TRANSFER_CLASS_1; 1.
.hylene blosynthesis; Lyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                         SNAGLFVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMD
                                   PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
1-aninocyclopropane-1-carboxylate synthase 1 (EC 4 4.1.14) (Ac
synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase)
                                                                                                   Length 485;
                                           A -> V (IN REF. 1; CAA41856).
L -> P (IN REF. 2).
P -> L (IN REF. 2).
P 40B3F55B5EF0D9C7 CRC64;
                                                                                                                   Indels
                                                                                                Ouery Match 66.9%; Score 1713; DB 1; Best Local Similarity 65.6%; Pred. No. 1.2e-124; Matches 319; Conservative 72; Mismatches 89;
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PS00105; AA_...
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                                           124
322
399
399
485 AA;
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       PROSITE; PS00105;
Fruit ripening; E
Multigene family.
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Q9MB95;
                                           CONFLICT
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CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
--- CATALYTIC ACTIVITY: S-adenosyl-L-methionine " 1-
aminocyclopropane-1-carboxylate + methylthioadenosine.
---- COFACTOR: PYRIDOXAL PHOSPHATE.
---- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
---- SUBUNIT: HOMODIMER (BY similarity).
---- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
AMINOTRANSFERASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
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                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB031026, BAA90549.1; -
InterPro: IPR001176; ACC_synthase.
InterPro: IPR00151; Aminotran_1.
Pfam; PF00155; aminotran_1.2; 1.
PRINTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
Fruit ripening; Ethylene blosynthesis; Lyase; Pyridoxal phosphate;
Multigene family. 277 PYRIDOXAL PHOSPHATE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDWILNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMSSFGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDELYAATVFSQPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PYRIDOXAL PHOSPHATE (BY SIMILARITY).
2002047AF2B43D89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.4%; Score 1698.5; DB 1; Length 492; Ilarity 66.6%; Pred. No. 1.6e-123; Conservative 62; Mismatches 86; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ŕ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55066 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             492 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 321; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 6
1A11_CUCMA
ID 1A11_CUCMA
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9
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDRIVMSGGATGAHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNN 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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01-NOV-1991 (Rel. 20, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase CMM33 (EC 4.4.1.14) (ACC 8971thase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
ACSI OR ACCW.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS -1- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDUCTION: BY TISSUE WOUNDING. SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MGFKAMDQ--TPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRIDOXAL PHOSPHATE (BY S F39234AC99CBEF6B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.1%; Score 1640.5; DB 1;
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                                                                                                                                                                                                       Cucurbita maxima (Pumpkin) (Winter squash).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P37821; 1B8G.
Mendel; 244; CUCMa;Acs;1.
InterPro; IPR001176; ACC_synthase.
InterPro; IPR001511; Aminotran_1.
Pfam; PF00155; aminotran_1.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: PYRIDOXAL PHOSPHATE.
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                                                                                                                                                                                                                                                                                                  eurosids I; Cucu
NCBI_TaxID=3661;
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Best Local S.
Matches 313
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SOURCE STANDARD BRANCH STANDARD SOURCE STANDARD SOURCE SOU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91139670; PubMed=1995630; Sato T., Oeller P.W., Theologis A.; "The l-aminocyclopropane-1-carboxylate synthase of Cucurbita. Purification, properties, expression in Escherichia coli, and primary structure determination by DNA sequence analysis."; J. Biol. Chem. 266:3752-3759(1991).
                                                                                                                             LOSNAGLEVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYAN 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cucurbita pepo (Vegetable marrow) (Summer squash).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
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                                                                                                                                                                           MDDMAVQIALQRIRNFV -- LQNKE---VVVSNKKHCWHSNLRL--SLKTRRFDD--ITMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-91334397; PubMed-1871117;
Huang P.-L., Parks J.E., Rottman W.H., Theologis A.;
Two genes encoding 1-aminocyclopropane-1-carboxylate synthase in
zucchini (Cucurbita pepo) are clustered and similar but
differentially regulated.";
                                                                                                                                                                                                                                                                                                                                                                                                                                      (EC 4.4.1.14) (ACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 88:7021-7025(1991).
-!- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                     synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1991 (Rel. 20, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase 1
                                                                                                                                                                                                                                                                                                                                                       493 AA.
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                                                                                                                                                                                                                                                                       PHTMSPHSPLVIAKN 493
                                                                                                                                                                                                                                         470 PHSPLPQSPMVKATN 484
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01-NOV-1991
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MEDLINE-91334397; PubMed-1871117;
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                                                                                                                                                                                                                                                                                                                                                                                                            469
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Eukaryota, Viridiphantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
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                                                                                                                                                                                                                                                61 SFDMIVDWIRKHPEASICTPEGLERFKSIANFQDYHGLPEFRNAIANFWGKVRGGRVKFD 120
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                                                                                                                                                                          13;
                                                                                                                                                     64.0%; Score 1637.5; DB 1; Length 493; 63.0%; Pred. No. 8.1e-119; Live 74; Mismatches 96; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IAIZ_CUCPE STANDARD; PRT; 494 AA.
000379;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase 2 (EC 4.4.1.14) (ACC synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
                                                                           Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal Multigene family.

BINDING 279 279 PYRIDOXAL PHOSPHATE.
                                                                                                             -> R (IN REF. 2).
921DC3DFB17A8769 CRC64;
                 HSSP, P3781; IB8G.
InterPro; IPR001176; ACC_synthase.
InterPro; IPR00115; Aniotran_1.
Pfan; PF00155; aminotran_1.2; 1.
PRINTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
                                                                                                              v
                                                                                                                       493 AA; 55779 MW;
                                                                                                                                                                         312; Conservative
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PHTMSPHSPLVIAKN 493
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                                                                                                                                                                Similarity
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SEQUENCE FROM N.A.
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                                                                                                                                                    Query Match
Best Local Si
Matches 312;
                                                                                                            CONFLICT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                       SEGMIVDWIRKHPEASICTPEGLEKEKSIANFQDYHGLQEFRKAMASFMGKVRGGRVKFD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mendel; 247; CUCpe; Acs; 2.
InterPro; IPR001176; ACC_synthase.
InterPro; IPR00151; Aminotran_1.
Pfam; PF00155; ACCSTNTHASE.
PROSITE; PR00753; ACCSTNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
Fruit ripening; Ethylene blosynthesis; Lyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VRRARQMSSFGLVSSQTQHLLAAMLSDEDFVDKFLAENSKRLGERHARFTKELDKMGITC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PYRIDOXAL PHOSPHATE (BY SIMILARITY).
A -> AS (IN REF. 1; AAA33112).
02AE029AA4912C36 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVLTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCD
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Huang P., Parks J.E., Rottman W.H., Theologis A.;
"Two genes encoding 1-aminocyclopropane-1-carboxylate synthase succhini (Qucurbita pepo) are clustered and similar but differentially regulated";
Proc. Natl. Acad. Sci. U.S.A. 88:7021-7025(1991).
-I- FUNCTION: CATALXZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63.6%; Score 1627.5; DB 1; Length 494;
Llarity 63.1%; Pred. No. 4.8e-118;
Conservative 73; Mismatches 96; Indels 13;
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55922 MW;
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494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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BINDING 279
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Best Local Simil
Matches 311; (
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MGSYKGVYDREILSKIATNDGHGENLEYFDGWKAYDRDPYHSTKNSNGVIQMGLAENQLC
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                                Park K.Y., Drory A., Woodson W.R.;

"Molecular cloning of an 1-aminocyclopropane-1-carboxylate synthase from senescing carnation flower petals.";

Plant Mol. Biol. 18:377-386(1992).

-!- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.

-!- CATALYTIC ACTIVITY: S-adenosyl.L.methylthioadenosine.

-!- COFACTOR: PYREDOXAL PHOSPHATE.

-!- PATHWAY: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.

-!- SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
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HSSP, P37821, 188G.
InterPro; PR001176, ACC_synthase.
InterPro; IPR001511, Aminotran_1.
Pfam; PF00155, aminotran_1_2; 1.
PRINTS; PR00755, ACCSYNTHASE.
PROSTIE; PS00105; AA_TRANSFER_CLASS_1; 1.
Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                        Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Caryophyllaceae; Dianthus. NCBL_TaxID-3570;
             MDDMAVQIALQRIRNFV -- LQNKE---VVVSNKKHCWHSNLRL--SLKTRRFD--DITMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PYRIDOXAL PHOSPHATE (BY SIMILARITY)
                                                                                                                                                                                                                                          01-AUG-1992 (Rel. 23, Last sequence update)
15-DEC-1998 (Rel. 37, Last annocation update)
1-aminocyclopropanel-carboxylate synthase (EC 4.4.1.14) (ACC synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C31BA10732E940AE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 62.7%; Score 1603.5; DB 1
Best Local Similarity 58.5%; Pred. No. 3.6e-116;
Matches 303; Conservative 80; Mismatches 96;
                                                                                                                                                                                                                                                                                                                        Dianthus caryophyllus (Carnation) (Clove pink)
                                                                                                                                                                                            517 AA.
                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-92119258; PubMed-1731995;
                                                                                                                                                                                                                              (Rel. 23, Created)
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                                                                                                                                                                                             STANDARD:
                                                                            470 PHSPLPQSPMVKA 482
                                                                                              ||: | ||:|:|
PHTMSPHSPLVRA 491
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517 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                          1A1C_DIACA
P27486;
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STARRMSSFGLVSSQTQFWIAALLSDDDFVRRFLVESRDRLFRRHQHFTSELAKIGIGCL 357
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                                           420 DDMAVQIALQRIRNFVLQNK-------EVVVSNKKHCWH 451
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STRAIN-CV. CARUSO; TISSUE-Etiolated hypocotyl;
MEDLINE-93374928; bubMed-8366090;
Lincoln J.E., Campbell A.D., Oetiker J., Rottmann W.H., Oeller P.W., Shen N.F., Theologis A.,
"LE-ACS4, a fruit ripening and wound-induced l-aminocyclopropane-1-carboxylate synthase gene of tomato (Lycopersion seculentum).
Expression in Escherichia coli, structural characterization, expression characteristics, and phylogenetic analysis.";
J. Blol. Chem. 268:19422-19430(1993).
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                                                                                                                                                                                                         121 DRIVMSGGAS-ASETLLFCLANPGDAFLIPSPYYPAFNRDLRWRTGVNLIPFTCSSSNNF
                                                                                                                                                                                                                                                                                                                                                                                   SDLVEDWILNNPEASICTPEGINDFRAIANFODYHGLAEFRNAVAKFMARTRGNRITFDP
                                                                                                                                                                      DRIVMSGGATGAHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNF
                                                                                                                                                                                                                                                                                                                                   180 VLTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 IYAATVFSQPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             360 OSNAGLFVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANM
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1.5.DEC-1998 (Rel. 37, Last annotation update)
1.aminocyclopropane-1-carboxylate synthase 4 (EC 4.4.1.14) (ACC synthase 4) (S-adenosyl-L-methionine methylthioadenosine-lyase 4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCARKMSSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 452 SNLRLSLKTRRFDD-----ITMSPHSPLPQSPMVKA
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MEDLINE-92106351; PubMed=1762159;
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J. Mol. Biol. 222:937-961(1991).
[3]
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ACS4 OR ACC4 OR PCVV4B.
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P29535;
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39; Gaps

96; Indels

Length 517;

1 MG-FKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLT

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MEDLINE-90280476; PubMed-191304;

A van der Straeten D., van Wiemeersch L., Goodman H.M., van Montagu M.;

A van der Straeten D., van Wiemeersch L., Goodman H.M., van Montagu M.;

A van der Straeten D., van Wiemeersch L., Goodman H.M., van Montagu M.;

A van der Straeten D., van Wiemeersch L., Goodman H.M., van Montagu M.;

A van der Straeten D., van Wiemeersch L., Goodman H.M., van Montagu M.;

A van der Straeten D., van Wiemeersch L., Goodman H.M., van Montagu M.;

A van der Straeten D., van Wiemeersch L., Goodman H.M., van Montagu M.;

A van der Straeten D., van Wiemeersch L., Goodman H.M., van Montagu M.;

A van der Straeten D., van Wiemeersch L., Goodman H.M., van Montagu M.;

A van der Straeten D., van Wiemeersch L., Goodman H.M., van Montagu M.;

A van der Straeten D., van Woodman H.M., van Montagu M.;

A van der Straeten D., van Montagu M.;

A van der Straeten D., van Montagu M.;

A van Montagu M.;

A van der Straeten D., van Montagu M.;

A van 
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InterPro; IPR001511; AmInotran_1.
Pfam; PF000155; aminotran_1_2; 1.
PRINS; PR00155; ACCSYNTHASE.
PROSTIE; PS00105; AA_TRANSFER_CLASS_1; 1.
Fruit ripening; Ethylene blosynthesis; Lyase; Pyridoxal phosphate;
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SEQUENCE FROM N.A.
MEDLINE-91271385; PubMed-1711229;
Olson D.C., White J.A., Reelman L., Harkins R.N., Kende H.;
Differential expression of two genes for 1-aminocyclopropane-1-carboxylate synthase in tomato fruits.";
Proc. Natl. Acad. Sci. U.S.A. 88:5340-5344(1991).
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T -> A (IN REF. 4).
S -> P (IN REF. 2).
9BC7D97BD64CBO44 CRC64;
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EMBL, X59146; CAA41857.1; --
EMBL, M63490; AAA34131.1; --
EMBL, M38705; AAA34131.1; --
EMBL, M38705; AAA34131.1; --
PIR, A40960; A40960
PIR, S19679; S19679.
HSSP, P37821; 1886.
Mendel; 511; LYCes; ACS;4.
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SEQUENCE OF 20-159 FROM N.A.
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253 253
476 AA; 53537 M
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BINDING 282
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Matches
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STRAIN-CY. COLUMBIA,
MEDLINE-21016719; PubMed-11130712;
Theologis A., Ecker J. R., Palm C.J., Federspiel N.A., Kaul S.,
Theologis A., Lacker J. Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.B., Er, J.H., Dewar K.,
Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Feng B., Fujii C.Y.,
Glil J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
Kim C.J., Koo H.L., Kremenetskala I., Kurtz D.B., Kwan A., Lam B.,
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
Millitscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV. COLUMBIA;
MEDLINE-93028584; Pubwed-1357670;
van der Straeten D., Rodrigues-Pousada R.A., Villarroel R., Hanley S.,
Goodman H.M., van Montagu M.;
"Cloning, genetic mapping, and expression analysis of an Arabidopsis
thallana gene that encodes 1-aminocyclopropane-1-carboxylate
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311 VSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD
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STRAIN-CV. COLUMBIA;
Terryn N.;
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                                                                                                                                                                                                                                                                                                                                                                               -1- COFACTÓR: PYRÍDOXAL PHOSPHATE.
-1- PATHWAT: FIRST, AND RATE LIMITING STEP OF ETHYLENE BIOSYNTHESIS.
-1- SUBBNIT: HOMODIMER.
-1- TISSUE SPECIFICITY: HIGH IN DEVELOPING LEAVES AND IN FLOWERS.
Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D., Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M., Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D., Utterback T., Van Aken S., Vaysberg M., Vysotskala V.S., Walker M., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.; "Sequence and analysis of chromosome 1 of the plant Arabidopsis thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfan; PF00155; aminotran_1_2; 1.
PRINTS; PR00753; ACCSYNTHARE.
PROSITE; PS00105; AA_TRANSFER.
Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
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                                                                                                                                                                                                                   Nature 408:816-820(2000).
-!- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-CARBOXYLATE, A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-aminocyclopropane-1-carboxylate + methylthioadenosine.
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HISP: P37821; 188G.
Mendel: 15544; ARAth; Acs; mn15544.
InterPro; IPR001176; ACC_synthase.
InterPro; IPR001511; Aminotran_1.
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EMBL; M95594; AAA97516.1; -.
EMBL; Y12776; CAA73310.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AC061957; AAF81308.1;
PIR; S31646.
PIR; A47199; A47199.
PIR; S46190; S46190.
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"Cloning of a cDNA encoding 1-aminocyclopropane-1-carboxylate synthase and expression of its mRNA in ripening apple fruit."; Planta 185:38-45(1991).
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CARKMSSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Malus domestica (Apple) (Malus sylvestris).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Rosaceae; Maloideae, Malus.
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STRAIN-CV. GOLDEN DELICIOUS; TISSUE-Fruit;
Dong J.G., Kim W.T., Yip W.K., Thompson G.A., Li L., Bennett A.B.,
Yang S.F.;
                                                                                                                                                                                                                                                                SNAGLEVWMDLRQLLK - KPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANM
                                                                                                                                             DDMAVQIALQRIRNFVLQNKEVVV------SNKKHCW-HSNLRLSLKTRRFDD
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"A full-length cDNA encoding 1-aminocyclopropane-1-carboxylate
synthase from apple.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAIC_MALDO STANDARD; PRT; 473 AA.
P37821; Q40278; 004993;
01-0CT-1994 (Rel. 30, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (ACC synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
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Harada T., Sunako T., Sakuraba W., Goto S., Senda M., Akada
IShikawa R., Mizeti M.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. GOLDEN DELICIOUS; TISSUE-Fruit cortical tissue;
MEDLINE-95232185; PubMed-7716231;
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MEDLINE-20079531; Pubmed-10610793;
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SEQUENCE FROM N.A.
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                                                                                                                                                  FISIAEILEDETDIECDRN----LVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKM 305
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01-JUL-1993 (Rel. 26, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase CMA101 (EC 4.4.1.14) (ACC synthase) (S-adenosyl-L-methionine methylthioadenosine-lyase).
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-> K (IN REF. 3).
6ACA20759615E75D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52.4%; Score 1341; DB 1;
53.0%; Pred. No. 5.6e-96;
.1ve 83; M1smatches 126;
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Best Local Simi
Matches 251;
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Q00257;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Nakagawa N., Kamiya Y., Imaseki H.;

Nakagawa N., Kamiya Y., Imaseki H.;

Nuclectide sequence of an auxin-regulated l-aminocyclopropane-1-
carboxylic acid synthase gene from Cucurbita maxima Duch.";

(In) Plant Gene Register PGR5-110.

-I- FUNCTION: CATALYZES THE FORMATION OF 1-AMINOCYCLOPROPANE-1-
CARBOXYLAR: A DIRECT PRECURSOR OF ETHYLENE IN HIGHER PLANTS.

-I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine - 1-
aminocyclopropane-1-carboxylate + methylthioadenosine.

-I- COFACTOR: PYRIDOXAL PHOSPHATE.

-I- SUBUNIT: HOWODIMER.

-I- SUBUNIT: HOWODIMER.

-I- INDUCTION: BY TISSUE WOUNDING AND AUXIN.

AMINOTION: BY TISSUE WOUNDING TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT.
                                                                                                                                                                                                                  Nakagawa N., Mori H., Yamazaki K., Imaseki H.; "Cloning of a complementary DNA for auxin-induced 1-aminocyclopropane-1-carboxylate synthase and differential expression of the gene by
                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucurbita.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSGGATG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 LLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDWILNN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62

    Lyase; Pyridoxal phosphate;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDETYAATVFSQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PYRIDOXAL PHOSPHATE (BY SIMILARITY).
D02A666E137F44A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Cucurbita maxima (Pumpkin) (Winter squash)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P37821; 188G.
Mendel; 245; CUCma; Acs; 2.
InterPro; IPR001176; ACC.synthase.
InterPro; IPR001511; Aminotran_1.
Pfam; PF00155; aminotran_1.2; 1.
PRINTS; PR00753; ACCSYNTHASE.
PROSTTE; PS00105; AA_TRANSFER_CLASS_1; 1.
Fruit ripening; Ethylene biosynthesis; Lyk, Multigene family.
BINDING 272 PYRIDOXAL PHO
                                                                                                                                                                                                                                                                                                                                          Plant Cell Physiol. 32:1153-1163(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53481 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U37774; AAA91152.1; -. EMBL; D01033; BAA00839.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 55.39
Matches 246; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J02214; J02214.
                                                                                                                                                                                                                                                                                                      auxin and wounding."
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                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                    NCBI_TaxID-3661;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVW 368
                                                                                                                                                   361
                    FISIAEILEDET--DIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMSSF 308
                                                              301
                                                                                                                                                                                               MDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMDDMAVQIAL 428
                                                                                                                                                                                                                    362 VDMRHLLESDKFESELELWKKIVYEVGLNISPGSSCHCTEPGWFRVCFANMSESTLKLAV 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- INDUCTION: BY ANAEROBIOSIS AND INDOLEACETIC ACID (IAA) +
BENZYLADENINE (BA) + LICL TREATMENT.
-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P37821; 1B8G.
InterPro; IPR001176; ACC_synthase.
InterPro; IPR001511; Aminotran_1.
Prim; PF00155; aminotran_1.
PRIMIS; PR00753; ACCSYNTRASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
Fruit ripening; Ethylene biosynthesis; Lyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1994 (Rel. 30, Last sequence update)
1-OCT-1994 (Rel. 30, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase 1 (EC 4.4.1.14) (ACC synthase 1) (S-adenosyl-L-methionine methylthioadenosine-lyase 1).
                                                                                                                                 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                     QRIRNFVLQNKEVVVSNKKHCWHSN 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-1994 (Rel. 30, Created)
01-0CT-1994 (Rel. 30, Last seq
01-0CT-1994 (Rel. 30, Last anno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286
129
151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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BINDING 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                           1A11_ORYSA
Q07215;
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VARIANT
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                                                                                                                                                                                                                                                                                                                              123 VMSGGATGAHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLT 182
                                                                                                                                                                                                                                                                                                                                                                                                                         VVNCARKMSSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIK 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 CLQSNAGLFVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYA 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATVFSQP--GFISIAEILEDETDIEC---DRNLVHIVYSLSKDMGFPGFRVGIIYSYNDA 297
                                                                                                                                                                                                    5 AMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVE 64
                                                                                                                                                                                                                                7 AEERPQLISKRAGCNSHGQDSSYFLGWQEYEKNPFDPVSNPSGIIQMGLAENQLSFDLLE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- CATALYTIC ACTIVITY: L-aspartate + 2-oxoglutarate - oxaloacetate
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-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2001 (Rel. 40, Last annotation update)
Aspartate aminotransferase (EC 2.6.1.1) (Transaminase A) (ASPAT).
ASPC OR AQ_1969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber Feldman R.A., Short J.M., Olson G.J., Swanson R.V., "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                      6
                                                                                                     Length 487;
                                                                                                                                                      Indels
       G -> D.
90F8B0DEF3524009 CRC64;
                                                                                                     DB 1;
                                                                                                                            Pred. No. 1.3e-89; 77; Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Aquificales; Aquificaceae; Aquifex.
NCBL_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    394 AA
                                                                                                     Score 1258.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-VF5;
MEDLINE-98196666; PubMed-9537320;
                            53101 MW;
                                                                                              49.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          418 NMDDMAVQIALORIRNFV 435
                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 392:353-358(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          425 NMSAKTLDVAMORLRSFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMINOTRANSFERASES.
273 2
487 AA;
                                                                                                                            Best Local Similarity
Matches 236; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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067781:
       VARIANT
SEQUENCE
                                                                                                     Query Match
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                                                                           EMBL; AE000766; AAC07746.1; -.
HSSP; Q56232; 1BKG.
InterPro; IPR001376; ACC_Synthase.
InterPro; IPR001515; Aminotran_1.
Pfam; PF00155; aninotran_1.2; 1.
PRINTS; PR00753; ACCSYNTHASE.
PROSTIE; PS00105; AA_TRANSFER_CLAS_1; FALSE_NEG.
Transferase; Aminotransferase; Pyridoxal phosphate; Complete proteome. BINDING 239 PYRIOOXAL PHOSPHATE (BY SIMILARITY).
SEQUENCE 394 AA; 43777 MW; E570B4FD080C56E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 GGATGAHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEA 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDELYAATV 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             212 YGDAKEVSPAS-FSDEV----KNITFTVNAFSKSYSMTGWRIGYVACPEERAKVIASLN 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 MSSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKV-GIKCLQSNA 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    266 SQSVSNVTTFAQYGALEALKNPKSKD-FVNEMRNAFERRRDTAVEELSKIPGMDVVKPEG 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 GLEVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMDDMA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        325 AFYIFPDFSAYAEK--LGGDVKLSEFLLEKAKVAVVPGSAFGA--PGFLRLSYALSEERL 380
                                                                                                                                                                                                                                                                                                                                                                                                                                 72 EASICTPEGIND--FRAI----ANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 FSQPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYND-AVVNCARK 304
                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              41 EPDFDTPDFIKEACIRALREGKTKYAPSAGIPELREAIAEKLLKE--NKVEYKPSEIVVS 98
                                                                                                                                                                                                                                                                                                                                            Ouery Match 11.5%; Score 293.5; DB 1; Length 394; Best Local Similarity 25.5%; Pred. No. 2.5e-15; Matches 94; Conservative 75; Mismatches 171; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 VOIALORIR 432
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VE-GIRRIK 388
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Search completed: August 21, 2002, 02:12:11 Job time: 196 sec

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US-08-724-194-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 348;
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1 MGFKAMDQTPLLSKMAIGDG.......DITMSPHSPLPQSPMVKAIN 484
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/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                               Compugen Ltd
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US-08-378-313-31
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US-08-378-313-22
US-08-378-313-22
US-08-378-313-22
US-08-378-313-19
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              GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Maximum Match 100%
Listing first 45 summaries
                                                                            protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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US-08-724-194-6

Sequence 6, Application US/08724194

Patent No. 5848457

GENERAL INFORMATION:

APPLICANT: RANU, RAJINDER S.

TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE

TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS

TITLE OF INVENTION: IN GERANIUMS

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
         ILINNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSG 126
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US-09-412-184-40
US-08-59-171A-26
US-08-59-171A-26
US-08-646-590B-26
US-09-412-184-26
US-09-412-184-26
US-09-659-171A-29
US-09-659-171A-29
US-09-669-226-29
US-09-669-226-29
US-09-669-256-29
US-09-669-256-29
US-09-412-184-25
US-09-413-184-25
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Pred. No. 5e-200;
8; Mismatches 5
                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SANTANGELO LAW OFFICES PC
STREET: 315 WEST OAK STREET, STE 701
CITY: FORT COLLINS
STATE: CO
COUNTRY: USA
ZIP: 80521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,194
FILING DATE: 01-OCT-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SANTANGELO, LUKE
REGISTRATION NUMBER: 31,997
TELECOMUNICATION INFORMATION:
TELECHONE: (970) 224-3100
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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70.9%; Pred. No. 3.5e-194
tive 65; Mismatches 66
Best Local Similarity 70.9% Matches 339; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       69 VLNNPQASICTAQGLQEFKDTAIFQDYHGLQSSDMLFANFMGKVRGNRVTFNPDRIVMSG 128
                                  GATGAHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVP-VMCDSSNNFVLTKEA 185
                                                     FSQPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKM 305
                                                                                                                                                                                              249 FSQPAFVSIAEVIEQE-NVSCNRDLIHIVYSLSKDMGFPGFRVGIVYSYNDAVVNCARKM 307
                                                                                                                                                                                                                                             SSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGL 365
                                                                                                                                                                                                                                                                 FVWMDLRQLLKKPTFDSETELWKVITHEVKINVSPGYSFHCTEPGWFRVCYANMDDMAVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/08485107
Patent No. 5767376
GENERAL INFORMATION:
APPLICANT: STILES, JOHN I.
APPLICANT: NEUPAND, RABI R.
TITLE OF INFURNION: ACC SYNTHASE GENE AND ITS USE IN PLANTE NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 487;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,107
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ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: UH-01
TELECOMUNICATION INFORMATION:
TELEPHONE: (415,705-8410
TELEPHONE: (415,705-8410
TELEPHONE: (415,397-8338
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acids
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487 VRAT 490
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PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFWARTRGNRITFDPDRIVMSGGATG 130
                                                                                                                                                         131 AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY 190
                                                                                                                                                                                                                                           EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVFSQPG 250
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                                                                  10 LLSKIATSNGHGEDSPYFDGWKAYDSDPFHPTQNPEGVIQMGLAENQLCFNLIHEWLLKN 69
                                         LLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDWILNN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         431 IRNEVLQNKEVVVSNKKHCWHSNLRLSLKTRRFDDIT-----MSPHSPLPQSPMVKA 482
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| Sequence 31, Application US/08378313
| Patent No. 6207881
| GENERAL INFORMATION:
| APPLICANT: THEOLOGIS, ATHANASIOS
| TITLE OF INVENTION: GONTROL OF FRUIT RIPENING THROUGH
| TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
| NUMBER OF SEQUENCES: 34
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: MORRISON & FORRSTER
| STREET: 755 Page Mill Road
| CITY: Palo Alto
| STATE: California
| CONTRY: USA
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Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
FILING DATE:
CLASSIFICATION: 800
99
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PRICEATION NUMBER: US 07/862,493
PFILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,595
REFERENCE/DOCKET NUMBER: 29,190-20002.20
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 494-0792
TELEFAX: (415) 494-0792
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Query Match
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                                                                                                                                                                                                                                                              71 PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSGGATG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/08695412B
Patent No. 584269
GENERAL INFORMATION:
APPLICANT: STILES, JOHN I.
APPLICANT: MOISTADI, STEFAN
APPLICANT: NEUPANE, KABI R.
TITLE OF INVENTION: PURIFIED PROTEINS, RECOMBINANT
TITLE OF INVENTION: DNA SEQUENCES AND PROCESSES FOR CONTROLLING THE
TITLE OF INVENTION: RIPENING OF COFFEE
                                                                                                                                                                        Gaps
                                                                                                                                                                                                   11 LLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDWILNN 70
                                                                                                                                                                                                                    13 LLSKIATNDGHGENSPYFDGWKAYANNPFHLTDNPTGVIOMGLAENQLCFDLIQEWMVNN 72
                                                                                                                                                                        5.
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                                                                                                                                                                      66; Indels
                                                                                                                                      Query Match 69.2%; Score 1771.5; DB & Best Local Similarity 68.9%; Pred. No. 1.9e-188; Matches 326; Conservative 76; Mismatches 66,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: JONES, DAY, REAVIS & POGUE STREET: NORTH POINT, 901 LAKESIDE AVENUE CITY: CLEVELAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
MEDIUM TYPE: storage
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APPLICATION NUMBER: US/08/695,41
              SEQUENCE CHARACTERISTICS:
LENGTH: 483 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-378-313-31
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS ADDRESSE: JONES, DA
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67 ILNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVF 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLF 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 367 VWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMDDMAVQI 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 69.1%; Score 1768; DB 2; Best Local Similarity 67.1%; Pred. No. 4.8e-188; Matches 325; Conservative 83; Mismatches 66;
           CLASSIFICATION: *...
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/485,107
FILING DATE: 07-UNN-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRIFFITH, CALVIN P.
REFERENCE/DOCKET NUMBER: 26503660002
TELECOMONICATION INFORMATION:
TELEPHONE: (216) 586-7050
TELEPHONE: (216) 579-0212
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acid residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 30, Application US/08378313; Patent No. 6207881; GENERAL INFORMATION: APPLICANT: THEOLOGIS, ATHANASIOS; APPLICANT: SATO, TAKAHIDO
12-AUG-1996
                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: 178..1653
                                                                                                                                                                                                                                                                                                                                                             linear
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US-08-378-313-30
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DLVEDWILNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPD 120
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   431 ISYFVLQPKGLNNIAAIKKQCSRRKLQISLSFRRLDHEFMNSPAHSPM-NSPLVR 484
                                                                                                                                                    APPLICANT: THEOLOGIS, ATHANASIOS
APPLICANT: SATO, TAKAHIDO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
FILING DATE:
CLASSIFICATION: 800
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ilarity 65.6%; Pred. No. 6.4e-182;
Conservative 72; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-APR.1992
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REPERCECOCKET UMBER: 29,950
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 856-5600
TELEPHONE: (415) 494-0792
                                                                                               Sequence 27, Application US/08378313 Patent No. 6207881 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THE PC COMPATIBLE
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
TYPE: amino acids
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Best Local Similarity
Matches 319; Conserv
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                                                                             US-08-378-313-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        311 VSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131 AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7;
   CONTROL OF FRUIT RIPENING THROUGH
GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65; Indels
                                                                                                                                              COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.6%; Score 1755.5; DB 4 68.8%; Pred. No. 1.2e-186; Live 76; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-APR-1992
ATORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
RECISTRATION NUMBER: 29,959
RECISTRATION NUMBER: 29,959
TELECOMUNICATION INFORMATION:
TELECHORE: (415) 856-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :-
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                                                                       ADDRESSEE: MORRISON & FOERSTER STREET: 755 Page Mill Road CITY: Palo Alto STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAA: V. TELEFAA: V. TELEEX: 706141
INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS: LENGTH: 485 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
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Best Local Similarity 68.8%
Matches 327; Conservative
TITLE OF INVENTION: CONTITLE OF INVENTION: GEN NUMBER OF SEQUENCES: 34 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                             FILING DATE:
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TOPOLOGY:
US-08-378-313-30
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RIVMSGGATGAHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFV 180
                                                                LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEI 240
                                                                                                                                                                                                       241 YAATVFSQPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVN 300
                                                                                                                                                                                                                            240 YAATVEDTPQFVSIAEILDEQEMTYCNKDLVHIVYSLSKDMGLPGFRVGIIYSFNDDVVN 299
                                                                                                                                                                                                                                                                                    301 CARKMSSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQ 360
                                                                                                                                                                                                                                                                                                        DLIEDWIKRNPKGSICS-EGIKSFKAIANFQDYHGLPEFRKAIAKFMEKTRGGRVRFDPE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                             421 DMAVQIALQRIRNFVLQNKEVVVSN---KKHCW-HSNLRLSLKTRRFDDITMSP-HSPLP 475
                                                                                                                                                                                                                                                                                                                                                                 SNAGLFVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25, Application US/08378313
Patent No. 6207881
GENERAL INFORMATION:
APPLICANT: THEOLOGIS, ATHANASIOS
APPLICANT: SATO, TAKAHIDO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29190-20002.20
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILLING DATE: 02-ARR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: MORRISON & FOERSTER 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/Ms-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REERENCE/DOCKET NUMBER: 291
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (415) 856-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 485 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (415) 494-0792
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CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
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COMPUTER READABLE FORM:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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US-08-378-313-25
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301 CARKMSSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQ 360
                      420
                                                                                                     360 NNAGLECWADLRPLIRESTEDSEMSLWRVIINDVKLNVSPGSSFECQEPGWFRVCFANMD 419
                                                                                                                                                           421 DMAVQIALQRIRNFVLQNKEVVVSN---KKHCW-HSNLRLSLKTRRFDDITMSP-HSPLP 475
                                                                                                                                                                                  61 DLVEDWILNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPD 120
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                                                                            361 SNAGLEVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMD
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Patent No. 6207881

GENERAL INFORMATION:
GAPPLICANT: THEOLOGIS, ATHANASIOS
APPLICANT: SATO, TAKAHIDO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCES: MORRESON & FORESTER
ADDRESSEE: MORRESON & FORESTER
STREET: 755 PAGE Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 485;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.9%; Score 1713; DB 4;
65.6%; Pred. No. 6.4e-182;
11ve 72; Mismatches 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29190-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 856-5600
TELEPAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-ARR-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 485 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 66.9
Best Local Similarity 65.6
Matches 319; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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US-08-378-313-32
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REGISTRATION NUMBER: 31,997
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US-08-724-194-5
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APPLICANT: RANU, RAJINDER S.
TITLE OF INVENTION: ONB-AMINOCYCLOPROPANE-1-CARBOXXLATE
TITLE OF INVENTION: SYNTHASE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS
TITLE OF INVENTION: 11 GERANIUMS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                    4
                                                                                                                                                                                                                  DLVEDWILNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPD 120
                                                                                                                                                                              61 DLIEDWIKRNPKGSICS-EGIKSFKAIANFQDYHGLPEFRKAIAKFWEKTRGGRVRFDPE 119
                                                                                                                                                                                                                                                                        LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEI 240
                                                                                                                                                                                                                                                                                      241 YAATVFSQPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVN 300
                                                                                                                                                                                                                                                                                                                                         CARKMSSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQ 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DMAVQIALQRIRNEVLQNKEVVVSN---KKHCW-HSNLRLSLKTRRFDDITMSP-HSPLP 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                        1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTS 60
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                                                        Length 485;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC CompALIA-E
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,194
FILING DATE: 01-OCT-1996
CLASSIFICATION: 800
                                                    66.8%; Score 1710; DB 4;
65.6%; Pred. No. 1.4e-181;
clve 71; Mismatches 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SANTANDELO LAW OFFICES PC
STREET: 315 WEST OAK STREET, STE 701
CITY: FORT COLLINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08724194
Patent No. 5824875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: SANTANGELO, LUKE
                                                     Query Match
Best Local Similarity 65.6
Matches 319; Conservative
protein
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 ; MOLECULE TYPE:
US-08-378-313-25
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COUNTRY: US
ZIP: 80521
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US-08-724-194-5
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GENERAL INFORMATION:

APPLICANT: RANJ, RAJINDER S.

APPLICANT: RANJ, RAJINDER S.

TITLE OF INVENTION: ONE-AMINOCYCLOPROPANE-1-CARBOXYLATE

TITLE OF INVENTION: SYNTHAE GENES FROM PELARGONIUM TO CONTROL ETHYLENE LEVELS

TITLE OF INVENTION: IN GERANIUMS

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: SANTANGELO LAW OFFICES PC

STREET: STREET, STE 701

CITY: FORT COLLINS

STREET: CO.
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                                                                                                                                                                                                                                                                            3,
                                                                                                                                                                                                                                     Length 482;
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                                                                                                                                                                                                                                     DB 2;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                66.5%; Score 1702.5; DB 2; 65.8%; Pred. No. 9.3e-181; iive 85; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/724,194
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; Sequence 4, Application US/08724194
; Patent No. 5824875
             TELEPHONE: (970) 224-3100
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 482 amino acids
TYPE: amino acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                   Query Match
Best Local Similarity 65.8
Matches 312; Conservative
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                         FILING DATE
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APPLICANT: STATO, TAKAHIDO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSE: MORRISON & FORESTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                            Length 482;
                                                                                                                                                                                                                                                      75; Indels
                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                         66.4%; Score 1698.5; DB 265.6%; Pred. No. 2.6e-180; ive 85; Mismatches 75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 19, Application US/08378313
Patent No. 6207881
GENERAL INFORMATION:
       CLASSIFICATION: 800
ATORNEY/AGENT INFORMATION:
NAME: SANTANGELO, LUKE
REGISTRATION NUMBER: 31,997
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 224-3100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 482 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
01-OCT-1996
                                                                                                                                                                                                                         Query Match 66.49
Best Local Similarity 65.69
Matches 311; Conservative
                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Palo Alto
STATE: California
                                                                                                                                                                 ; TOPOLOGY: linear
US-08-724-194-4
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FILING DATE:
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359 LQSNAGLEVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYAN 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIYAATVFSQPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAV 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          119 MDDMAVQIALQRIRNFV--LQNKE---VVVSNKKHCWHSNLRL--SLKTRRFDD--ITMS 469
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 FVLTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64.0%; Score 1637.5; DB 4; Length 493; 63.0%; Pred. No. 1.7e-173; ive 74; Mismatches 96; Indels 13;
PatentIn Release #1.0, Version #1.25
                                                                                    CLASSIFICATION B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 02 07/862,493
FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MORASHICE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,31:
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GENERAL INFORMATION:
APPLICANT: THEOLOGIS, ATHANASIOS
                                                                                                                                                                                                                                                                                                                                                    TELEX: 706141
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 856-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 493 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 63.0
Matches 312; Conservative
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59 TSDLVEDWILNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFD 118
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                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: THEOLOGIS, ATHANASIOS
APPLICANT: STO, TAKAHIDO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.0%; Score 1636.5; DB 4; Length 493; 63.0%; Pred. No. 2.2e-173; Live 74; Mismatches 96; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94304-1018
COMPUTER, READABLE FORM:
CMEDION TYPE: Floppy disk
CMEDION TYPE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                          RESULT 13
US-08-378-313-28
; Sequence 28, Application US/08378313
; Patent No. 6207881
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TELEPHONE: (415) 856-5600
TELEFAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 493 amino acids TYPE: amino acid
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Best Local Similarity 63.09
Matches 312; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   479 PHTMSPHSPLVIAKN 493
                                                                                             470 PHSPLPQSPMVKATN 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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US-08-378-313-28
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APPLICANT: SATO, TAKAHIDO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 493;
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                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMENT RELEASE #1.0, VERSION #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
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63.0%; Pred. No. 2.2e-173;
tive 74; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: WURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 856-5600
TELEPHONE: (415) 494-0792
                                                                                                                                             ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 493 amino acids
TYPE: amino acid
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                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 800
                                                                                                                                                                                 STA...
STATE: Califor...
COUNTRY: USA
TO: 94304-1018
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Matches 312; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                              359 LOSNAGLFVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYAN 418
                                                                                                                                             419 MDDMAVQIALQRIRNFV--LQNKE---VVVSNKKHCWHSNLRL--SLKTRRFDD--ITMS 469
239 EIYAATVFSQPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAV 298
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APPLICANT: SATO, TAKAHIDO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONFROL OF ACC SYNTHASE SYNTHESIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORENTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63.6%; Score 1627.5; DB 4; Length 494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 02 07/862,493
FILING DATE: 02-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: MUNASHIGE, KATE H.
RESISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 29,959
TELECHONE: (415) 856-5600
TELECHONE: (415) 494-0792
TELEFAX: 706141
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-08-378-313-23
; Sequence 23, Application US/08378313
; Patent No. 6207881
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Matches 311; Conservative
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ZIP: 94304-1018
COMPUTER READABLE FORM:
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STATE: California
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1 MGFKAMDQ--TPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQL 58

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LOSNAGLFVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYAN 418
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                                                                                                                                                  119 PDRIVMSGGATGAHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNN 178
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EIYAATVFSQPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAV
                                                                                                                                                                                                                                     179 FVLTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCD
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APPLICANT: SATO, TAKAHIDO
TITLE OF INVENTION: CONTROL OF FRUIT RIPENING THROUGH
TITLE OF INVENTION: GENETIC CONTROL OF ACC SYNTHASE SYNTHESIS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHILIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 29,959
PERERENCE/POCKEY NUMBER: 29190-20002.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 856-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/862,493
FILING DATE: 02-APR-1992
ATTORNEY AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 29, Application US/08378313 Patent No. 6207881 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (415) 494-0792
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CLASSIFICATION: 800
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TELEX: 7
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                                                                                                                                                                         1 MGFKAMDQ--TPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQL 58
                                                                                                                                                   13;
                                                                                                                       DB 4; Length 494;
                                                                                                                                                   Indels
                                                                                                                                                  96;
                                                                                                                      Query Match 63.6%; Score 1627.5; DB 4. Best Local Similarity 63.1%; Pred. No. 2.2e-172; Matches 311; Conservative 73; Mismatches 96;
; INFORMATION FOR SEQ ID NO: 29; SEQUENCE CHEMACTERISTICS:
; LENGTH: 494 amino acids; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-378-313-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHSPLPQSPMVKA 482
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PHTMSPHSPLVRA 491
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Search completed: August 21, 2002, 02:08:53 Job time: 4743 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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 protein search, using sw model protein æ

Run on:

August 21, 2002, 02:01:05; Search time 42.72 Seconds (without alignments) 1088.653 Million cell updates/sec

Title: Perfect score:

US-09-763-957-2 2559 1 MGFRAMDQTPLLSKWAIGDG......DITMSPHSPLPQSPMVKAIN 484 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 seqs, 96089334 residues Searched:

283138 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
!: pir4:*

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	1-aminocyclopropan	1-aminocyclopropan	1-aminocýclopropan	1-aminocyclopropan	1-aminocýclopropan	1-aminocyclopropan																							
SUMMARIES	ai	S26214	. \$25002	T06253	T02249	T07601	T07596	T04315	T03978	S31450	T50552	T13019	S19677	T50551	T09734	S48827	JQ0926	T09658	A41141	T47943	B41141	S56695	S31442	S71583	S19252	S19679	A47199	T10513	T08119	S52283
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	Match Length	484	484	487	483	483	485	477	491	490	487	495	485	477	488	491	493	493	493	488	464	455	518	486	516	476	496	370	421	363
a C	Match	100.0	92.0	82.7	70.0	9.69	68.4	68.3	•	67.3	67.2	67.1	6.99	8.99	999	65.1	•	÷	4	63.8	63.6	63.6	63.3	62.1	ď.	61.9	61.7	59.4	٠.	56.9
	Score	2559	2354	2115.5	1791.5	1781.5	1750.5	1747.5	1739.5	1721	1719.5	1716	1713	1709.5	1701.5	1667	1640.5	1640.5	1636.5	1635.5	1627.5	1626.5	1620	1588.5	1587	1583	1578		œ.	1455
Result	No.	1	7	m	4	S	φ	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

1-aminocyclopropan 1-aminocyclopropan	1-aminocyclopropan 1-aminocyclopropan	1-aminocyclopropan 1-aminocyclopropan	1-aminocyclopropan									
T07827 T17017	S52635 T10854	T06024 S54012	T16999	J02214	S56176	T10889	T17018	S47049	T06004	T06252	A57540	871174
77	77	~ ~	7	7	ď	Н	7	~	7	~	Н	7
366 364	373 467	469	473	475	465	472	446	441	447	480	469	470
56.1 55.0	54.3 52.9	52.5 52.4	52.4	52.3	52.2	52.0	51.4	51.3	51.2	51.2	50.8	9.09
1435	1390.5 1354.5	1343.5 1341	1341	1339.5	1335	1329.5	1316.5	1314	1309	1309	1299	1295.5
30	33 33	34 35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 (100 d) 526214	
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (clone pAIM-1) - mung bean	4.1.14) (clone pAIM-1) - mung bean
N; Alternate names: ACC synthase	
C;Species: Vigna radiata (mung bean)	
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 03-Dec-1999	15 #text_change 03-Dec-1999
C; Accession: S26214; S26213; S20919	•
R; Botella, J.R.; Arteca, J.M.; Schlagnhaufer, C.D.; Arteca, R.N.; Phillips, A.T.	 Arteca, R.N.; Phillips, A.T.
Plant Mol. Biol. 20, 425-436, 1992	•
A/Title: Identification and characterization of a full-length cDNA encoding for an au	full-length cDNA encoding for an au
of its mRNA in response to indole-3-acetic acid.	
A; Reference number: S26213; MUID:93043033	
A; Accession: S26214	
A; Molecule type: mRNA	
A; Residues: 1-484 <bot></bot>	
A; Cross-references: EMBL: 211613; NID: q22069; PIDN: CAA77688, 1; PID: q22070	1:CAA77688.1; PID:q22070
A; Experimental source: clone pAIM-1	•
A; Accession: S26213	
A; Status: nucleic acid sequence not shown; translation not shown	ation not shown
A; Molecule type: mRNA	
A; Residues: 50-415, 'F', 417 <bow></bow>	
A; Cross-references: EMBL: 211562; NID: q22067; PIDN: CAA77655.1; PID: q22068	1:CAA77655.1; PID:q22068
A; Experimental source: clone pHIM-1	
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1992	the EMBL Data Library, January 1992
R; Botella, J.R.; Schlagnhaufer, C.D.; Arteca, R.N.; Phillips, A.T.	I.; Phillips, A.T.
Plant Mol. Biol. 18, 793-797, 1992	
A; Title: Identification and characterization of three putative genes for 1-aminocyclo	three putative genes for 1-aminocyclo
A; Reference number: S20919; MUID:92216056	
A; Accession: S20919	
A; Molecule type: DNA	
3 - Boot discr. 27 - 64 JBOBS	

A; Residues: 27-94 <BOF>

A)Cross-references: GB:M80554; NID:g170628; PIDN:AAA53297.1; PID:g170632
A)Experimental source: Rwilcz cv. Berken, etiolated hypocotyls; clone pMAC-1
C; Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C; Keywords: carbon-sulfur lyase; ethylene blosynthesis; phosphoprotein; pyridoxal pho
F;279/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Gaps ö Length 484; Indels Query Match 100.0%; Score 2559; DB 2; Best Local Similarity 100.0%; Pred. No. 4.8e-196; Matches 484; Conservative 0; Mismatches 0;

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61 DLVEDWILNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPD 120 61 DLVEDWILLNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPD 120 à a

121 ò

RIVMSGGATGAHEVTAFCLADPGEAFLVPIPXYPGFDRDLRWRTGVKLVPVMCDSSNNFV 180

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encoding 1-aminocyclopropane-1-carboxylate
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C.Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C.Keywords: carbon-sulfur lyase; ethylene blosynthesis; phosphoprotein; pyridoxal
F:279/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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Best Local Similarity 81.1%;
Matches 394; Conservatiye 4
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                                                                                                                                                                                                                                                                                                                                                                         Traminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - soybean C; Species: Glycine max (soybean)
C; Species: Glycine max (soybean)
C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000
C; Accession: S25002
R; Liu, D.; Li, N.; Mattoo, A.K.
submitted to the RMEL Data Library, June 1992
A; Description: Nucleotide sequence of soybean ACC synthase.
A; Reference number: S25002
A; Reference number: S25002
A; Reference number: S25002
A; Recession: S25002
A; Residues: 1-484 < LIU>
A; Cross-references: EMBL: X67100; NID:gl8557; PIDN:CAA47474.1; PID:gl8558
C; Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C; Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C; Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C; Keywords: carbon-sulfur lyase; ethylene blosynthesis; phosphoprotein; pyridoxal p; 279/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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 RIVMSGGATGAHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFV
                          LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEI
                                       SNAGLEVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMD
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C;Accession: T07596
R;Cono, Y.; Nguyen, M.D.; Hennig, L.; Yu, G.; Rottoman, W.H.; Campbell, A.D.; Lincoln submitted to the EMBL Data Library, September 1996
A;Bescription: LE-ACSIA and LE-ACSIB, duplicated genes encoding 1-aminocyclopropane-1 A;Reference number: 216039
A;Reference number: 207596
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999 C;Accession: T07601
R;Cono, Y; Nguyen, M.D.; Hennig, L.; Yu, G.; Rottoman, W.H.; Campbell, A.D.; Lincoln submitted to the EMBL Data Library, September 1996
A;Description: LE-ACSIA and LE-ACSIB, duplicated genes encoding 1-aminocyclopropane-1
                                                                                                                                                                                                                                                                                                                                                                                                                                         the conversion of S-adenosylmethionine to 1-aminocyclopropan
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N;Alternate names: ACC synthase; S-adenosyl-1-methionine methylthioadenosine-lyase
C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Pathway: ethylene biosynthesis
C;Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C;Reywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal
F;279/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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                                                                                                                                                                               A;Accession: T07601
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-483 < CON>
A;Cross-references: EMBL:U72390; NID:g1621642;
A;Experimental source: cultivar Rutgers; clone G;Genetics:
C;Genetics:
C;Function:
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Best Local Simi
Matches 327;
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C;Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C;Keywords: carbon-sulfur lyase; ethylene blosynthesis; phosphoprotein; pyridoxal phosph
F;278/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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N;Alternate names: ACC synthase; S-adenosyl-L-methionine methylthioadenosine-lyase
C;Species: Lycopersicon esculentum (tomato)
                                                                                                                                                                       1-daninocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - common tobacco (Species: Nicoriana tabacum (common tobacco) (Species: Nicoriana) 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 YAATIENKPDFISISEVIMEE-DVECDRDLIHIVYSLSKDLGFPGFRVGIIYSYNDVVTN 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         420
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68.1%; Pred. No. 7.5e-135;
iive 79; Mismatches 72; Indels
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Best Local Similarity 68.1<sup>s</sup>
Matches 329; Conservative
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                                       68.3%;
69.5%;
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                                     Query Match
Best Local Similarity
Matches 332; Conserv
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                                                                                                      conversion of S-adenosylmethionine to 1-aminocyclopropane-
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N;Alternate names: ACC synthase; S-adenosyl-L-methionine methylthioadenosine-lyase
C;Species: Lycopersicon esculentum (tomato)
C;bate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 16-Jun-2000
C;Accession: T04315
R;Nakajima, N.; Bae, G.; Saji, H.; Aono, M.; Kubo, A.; Kondo, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     enzymes
                                                                                                 A Description: catalyzes the conversion of S-adenosylmethionine to 1-aminocyclopro Py Pathway: ethylene blosynthesis
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C;Keywords: carbon-sulfur lyase; ethylene blosynthesis; phosphoprotein; pyridoxal F;279/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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;Superfamily: 1-aminocyclopropane-1-carboxylate synthase
;Keywords: carbon-sulfur lyase; ethylene blosynthesis; phosphoprotein; pyridoxal
;269/Binding site: pyridoxal phosphate (Lys) (covalent) *status predicted
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                   PID:91621641
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A;Description: Rapid accumulations of transcripts of ethylene biosynthesis A;Reference number: 215278
A;Reference number: 215278
A;Reference number: 215278
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                                                                                                                                                                                                                                                                                                               LLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDWILNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 485;
A;Cross-references: EMBL:072389; NID:g1621640; PIDN:AAB17278.1; A;Experimental source: cultivar Rutgers; clone pLEACS1A3 C;Genetics:
                                                                                                                                                                                                                                                             ee; Indels
                                                                                                                                                                                                                      68.4%; Score 1750.5; DB 1.
68.6%; Pred. No. 1.4e-131;
11ve 76; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-477 <NAK>
A; Cross-references: EMBL:AB013346; PIDN:BAA25916.1
A; Experimental source: tissue-type green leaves
C; Function:
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                                                                                                                                                                                                                                        Best Local Similarity be, or Matches 326; Conservative
                                                                   A; Gene: ACS1A
C; Function:
                                                                                                                                                                                                                            Query Match
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1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - common tobacco C;Species: Nicotiana tabacum (common tobacco)
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 31-Jan-2000
C;Accession: T03978
R;Bailey, B.A.; Avni, A.; Li, N.; Matoo, A.K.; Anderson, J.D.
Plant Physiol. 100, 1615-1616, 1993
A;Title: Nucleotide sequence of the Nicotiana tabacum cv Xanthi gene encoding 1-amino A;Reference number: 215173
A;Accession: T03978 pho 9 ŝ 310 430 300 190 182 VSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD 370 DLVEDWILINNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPD 120 Gaps Gaps 70 62 9 9 431 IRNFV-LQ-NKEVVVSNKK-HC-WHSNLRLSLKTRRFDDITMSPHSPLPQSPMVKATN 484 LLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDWILNN PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSGGATG 131 AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVFSQPG FISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMSSFGL LRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMDDMAVQIALQR MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTS 1 MGFENEKNSSILSKLATNEELGENSPYFDGWKAYDNDPFHPLKNPNGVIQMGLAENQLCF 6 7; Length 491; Indels Query Match 68.0%; Score 1739.5; DB 2; Best Local Similarity 66.5%; Pred. No. 1.1e-130; Matches 326; Conservative 71; Mismatches 84; Score 1747.5; DB Pred. No. 2.4e-131 66; Mismatches

	Db 300 CARKMSSFGLVSTQTQHLLAKMLSDEEFVANFLCESSMRLGKRHKHFTNGLEQVGIKCLK 359 Qy 361 SNAGLEVWMDLRQLLKKPTFDSETELWKVINHEVKINVSPGYSFHCTEPGWFRVCYANND 420
OY 421 DWAYQIALGATURFULQURE	C;Date: 12-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000 C;Accession: T50552 R;Accession: T50552 R;Accessio
RESULT 9 531450 Sald 50 Sald 50 Sald 50 Sald 50 Sald 50 C; Date: 22-Nov-1993 #Sequence_revision 10-Nov-1995 #text_change 04-Feb-2000 C; Date: 22-Nov-1993 #Sequence_revision 10-Nov-1995 #text_change 04-Feb-2000 C; Date: 22-Nov-1993 #Sequence_revision 10-Nov-1995 #text_change 04-Feb-2000 S; Date: 22-Nov-1993 #Sequence_revision 10-Nov-1995 #text_change 04-Feb-2000 R; Michael M. M.; Baudinette, S. C.; Savin, K. W.; Cobbett, C. S.; Cornish, E. C. Submitted to the EMBL Data Library, December 1992 A; Description: Isolation of petal senescence-associated cDNA clones encoding 1-aminocycl A; Reference number: S31450 A; Accession: S31450 A; Molecule type: MRNA	A; Rouscule Lype, DNA A; Residues: 1.407 < PBEK> A; Cross-references: EMBL:; C; Genetics: ASI A; Introns: 56/3; 100/3; 11 C; Function: A; Pathway: ethylene biosy; C; Superfamily: 1-aminocyc. C; Keywords: carbon-sulfur F; 277/Binding site: pyrid
C> MBL:218953; 1 ocyclopropane lfur lyase; e yridoxal phos	Query Match 67.2%; Score 1719.5; DB 2; Length 487; Best Local Similarity 66.3%; Pred. No. 4.2e-129; Matches 320; Conservative 74; Mismatches 74; Indels 15; Gaps 5; Qy 11 LLSKMAIGDGHGESSPYFDGWKAYDONPFHPTDNPNGVMQMGLAENOLTSDLVEDWILNN 70
Query Match 67.3%; Score 1721; DB 2; Length 490; Best Local Similarity 65.4%; Pred, No. 3.2e-129; Matches 320; Conservative 73; Mismatches 88; Indels 8; Gaps 4; Oy 1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMOMGLAENOLTS 60	
	131 AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVWCDSSNNFVLTKEALEDAY
QY 121 RIVMSGGATGAHEVTAFCLADPGBAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFV 180 1:1 1 1 :1	Db 190 NKAKEDNINVKGLIITNPSNPLGTTLDRETLKSLITFINENNIHLVCDEIYAATVFSSPS 249 Qy 251 FISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMSSFGL 310 :: ::::: :::
	Db 309 VSSQTQHMLASMLSDDSFVDKFLAESKRRIAKRHNIFSKVLEEVNITKFPSNAGLFCWMN 368 Qy 371 LRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMDDMAVQIALOR 430

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1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) 2 - tomato
N.Alternate names: ACC synthase; S-adenosyl-L-methionine methylthioadenosine-lyase
C.Specias: Lycopersicon esculentum (tomato)
C.Specias: Lycopersicon (1991)
C.Specias: Lycopersicon (1992)
A.Fitle: 1-aminocyclopropane-1-carboxylate synthase in tomato is encoded by a multige
A.Feference number: S19677; MUID:92106331
A.Feciasion: S19677
A.Fociasion: S19678
A.Feciasion: S24358; MUID:92339529
A.Fitle: A functional tomato ACC synthase expressed in Escherichia coli demonstrates
A.Feciasion: S24358
A.Feciasi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 9-488 clins
A; Residues: 9-488 clins
A; Cross-references: EMBL:X62536; NID:g19163; PIDN:CAA44397.1; PID:g19164
A; Reperimental source: cv. Pik Red
A; Reperimental source: cv. Pik Red
A; Reperimental source: cv. Pik Red
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
R; Yip, W.K.; Dong, J.G.; Kenny, J.W.; Thompson, G.A.; Yang, S.F.
R; Yan Data State Cerization and sequencing of the active site of 1-aminocyclopropane-1-A; Recession: B35201; MUD:91045911
A; Residues: 275-286 cYIP>
R; Yan Der Straten, D.; Van Wiemeersch, L.; Goodman, H.M.; Van Montagu, M.
A; Residues: 275-286 cYIP>
R; Yan Der Straten, D.; Van Wiemeersch, L.; Goodman, H.M.; Van Montagu, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 4853-4863, 1990
A; Title: Cloning and sequence of two different cDNAs encoding 1-aminocyclopropane-1-c
A; Residues: 275-286 cYIP>
R; Yan Der Straten, D.; Yan Wiemeersch, L.; Goodman, H.M.; Van Montagu, M.
A; Residues: 275-286 cYIP>
R; Yan Der Straten, D.; Yan William Straten, D.; Britle: Cloning and sequence of two different cDNAs encoding 1-aminocyclopropane-1-c
A; Recession: A35316
A; Molecule type: mRNA
A; Residues: 1-321, P; A; 333-998, L', 440-485 cvAn>
A; Cross references: GB:M34289; NID:92196141
A; Residues: 208-310 cv12>
A; Ritle: Differential accumulation of transcripts for four tomato 1-aminocyclopropane
A; Residues: 208-310 cv12>
A; Molecule type: mRNA
A; Res
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C.Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C.Keywords: carbon-sulfur lyase; ethylene blosynthesis; phosphoprotein; pyridoxal
F:278/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental
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ilarity 65.6%; Pred. No. 1.4e-128;
Conservative 72; Mismatches 89;
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Best Local Similarity
Matches 319; Conserv
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A:Introns: 60/3; 104/3; 158/2
C:Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C:Keywords: carbon-sulfur lyase; ethylene blosynthesis; phosphoprotein; pyridoxal phosph F:280/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                     l'aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) ACS-6 - Arabidopsis thaliana N.Alternate names: ACC synthase; protein FBL21.70 (Species: Arabidopsis thaliana (mouse-ear cress) (Species: Arabidopsis thaliana (mouse-ear cress) (Species: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 04-Feb-2000 (SAccession: T13019 *Sequence_revision 13-Aug-1999 #text_change 04-Feb-2000 (SAccession: T13019 *SA.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; M. Reference number: 217587 (A. Reference number: 217587 (A. Residues: 1-495 A. Residues: 1-
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IRNFVLQNKE-----VVVSNKKHCWHSNLRLSLK-TRRFDDITMSPHSPLPQSPMV
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66.8%; Pred. No. 8.2e-129;
11ve 59; Mismatches 89;
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Best Local Similarity 66.8%
Matches 322; Conservative
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Gene: ACS-6; ATSP:F8L21.70
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361 SNAGLEVWMDLRQLLKKPTEDSETELMKVIIHEVKINVSPGYSFHCTEDGWFRVCYANMD 360 NNAGLECWMDLRQLLKKPTEDSETELMKVIIHEVKINVSPGYSFHCTEDGWFRVCYANMD 421 DMAVQIALQRILARESTFDSEMSLMRVIINDYKLNVSPGSSFECQEGWFRVCFANMD 421 DMAVQIALQRIRNFVLONKEVVSN	RESULT 14 T09734 1-anthocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - papaya C;Species: Carica papaya (papaya) C;Species: Le'Jul-1999 #sequence_revision 16-Jul-1999 #text_change 20-Jun-2000 C;Accession: T09734 R;Lers, A.; Burd, S.; Sonego, L.; Khalchitski, A.; Lomaniec, E. A;Reference number: 216837 A;Accession: T09734
TSOSULT 13 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) acs2 [similarity] - sweet orang NiAlternate names: ACC synthase C;Species: Citrus sinensis (sweet orange) C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 03-Nov-2000 C;Accession: T5053 #squence_revision 21-Jul-2000 #text_change 03-Nov-2000 C;Accession: T5053 #squence_revision 21-Jul-2000 #text_change 03-Nov-2000 P;Wong, W.S.; Ning, W.; Xu, P.L.; Kung, S.D.; Yang, S.F.; Li, N.	A; Residues: 1-468 <lera #status="" (covalent)="" (lys)="" 1-aminocyclopropane-1-carboxylate="" 1-aminocyclopropane-1-carboxylate,="" 277="" a;="" binding="" biosynthesis="" biosynthesis;="" c;="" carbon-sulfur="" converts="" cross-references:="" description:="" embl:="" ethylene="" f;="" function:="" into="" keywords:="" lyase;="" pathway:="" pho="" phosphate="" phosphoprotein;="" predicted<="" pyridoxal="" s-adenosylmethionine="" site:="" superfamily:="" synthase="" td="" y11357=""></lera>
A;Title: Identification of two chilling-regulated 1-aminocyclopropane- 1-carboxylate syn A;Reference number: 225125 A;Accession: T50531 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Molecule type: mRNA A;Cross-references: EMBL:AJ012696; PIDN:CAB60831.1 C;Genetics: A;Cross-references: EMBL:AJ012696; PADN:CAB60831.1	Query Match 66.5%; Score 1701.5; DB 2; Length 488; Best Local Similarity 67.2%; Pred. No. 1.1e-127; Pred. Similarity 67.2%; Pred. No. 1.1e-127; Indels 9; Ga Matches 321; Conservative 68; Mismatches 80; Indels 9; Ga 11 LLSKMAIGDGGGESSPYFDGWRAYDQNPFHPTDNPNGYMQHAENQLASDLYEDWILNN 111111111111111111111111111111111111
C; Superfamily: 1-aminocyclopropane-1-carboxylate synthase C; Keywords: carbon-sulfur lyase; phosphoprotein; pyridoxal phosphate F; 268/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted Query Match Best Local Similarity 65.8%; Score 1709.5; DB 2; Length 477; Best Local Similarity 65.8%; Pred. No. 2.5e-128; Matches 314: Conservative 70: Mismatches 84: Indels 9: Gans 3:	Qy 71 PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFWARTRGNRITFDPDRIVWSGGATG 130
LLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVWQWGLAENQLTSDLVEDWILNN 70	QY 191 EKAREDNIRVKGLLITUPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVESOPG 250 : : : !

us-09-763-957-2.rpr

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Jeaninocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - wild cabbage ("Species: Brassica oleracea (wild cabbage) ("Species: 11-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000 ("Shacession: S4882) ("Species: Brassica to the EMBL Data Library, September 1994 ("Species to the EMBL S825) ("Species to the Embla Salation of a control of a con
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65.0%; Pred. No. 6.5e-125;
11ve 63; Mismatches 96;
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Phaseolus aureus (Mung bean) (Vigna radiata).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnollophyta; eudloctyledons; core eudlocts; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.
                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1-AMINOCYCLOPROPANE 1-CARBOXYLATE SYNTHASE (EC 4.4.1.14).
                                                                                                                                                                                                                                     484 AA
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                  Q9MB75
Q9S854
Q96579
P93235
Q94GA2
Q9SA24
O49123
O81636
                                                                            09SEJ9
09SXN9
09M7J6
09SUT3
09SLY6
09SYT9
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Q49819
Q65209
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Q43810
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09MB86
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 PRELIMINARY;
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1250.068 Million cell updates/sec
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                                            Search time 66.98 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries

    protein search, using sw model

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sp_invertebrate:*
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Searched:

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pisum sativ malus domes malus domes pelargonium Q43858 phaseolus a Description 022464 SUMMARIES 022464 09MB64 043858 ū DB Query Match Length 2559

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Phillips A.T.; "Identification and characterization of a full-length cDNA encoding for an auxin-induced 1-aminocyclopropane-1-carboxylate synthase from etiolated mung bean hypocotyl segments and expression of its mRNA in SEQUENCE FROM N.A.
STRAIN=RWILCZ, AND CV. BERKEN; TISSUE-ETIOLATED HYPOCOTYL;
MEDLINE-93043033; PubMed-1421146;
Botella J.R., Arteca J.M., Schlagnhaufer C.D., Arteca R.N.,

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Q9MB64
Q9MB64;
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                        Gaps
                                                                            1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTS 60
                                                                                                   [1] SEQUENCE FROM N.A. MEDIANE-98340552: PubMed-9675901; Peck S.C., Kende H.; Agene encoding 1-aminocyclopropane-1-carboxylate (ACC) synthase produces two transcripts: elucidation of a conserved response."; Plant J. 14:573-581(1998).
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Length 484;
                                        Indels
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1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.
Score 2559; DB 10;
Pred, No. 3.9e-195;
                                        Mismatches
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100.0%;
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                                      Matches 484; Conservative
                   Similarity
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481 KATN 484
Query Match
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ISOZYMES: A CYTOPLASMIC
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2010 (TrEMBLrel. 19, Last sequence update)
11-MINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.
MDACS-5B.
Malus domestica (Apple) (Malus sylvestris).
Malus domestica (Apple) (Streptophyta; Embryophyta; Esteryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I: Rosales; Rosaceae; Maloideae; Malus.
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-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- MISCELLANEOUS: IN EUKARYOTES THEMEN AND TATOCHOMDIRAL ONE (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DLVEDWILNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAATVFSQPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 SNAGLFVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DMAVQIALQRIRNFVLQ-NKEVVVS--NKKHCWHSNLRLSLKTRRFDDITMSPHSPLPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            421 DRDVQIALQRIRSFVTQNNKEAMGSDKNSKPYWHSNLRLSLKPRRFDDIMMSPHSPIPQS
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                                                                                                                                                                                                                                                                                                                                                                          Length 487;
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                                                                                                                                                                                                                                                                                                                                                                                                                        42; Indels
                                                                                                                                                                                                                                                                                                       55116 MW; 8485B1DB38497634 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        82.7%; Score 2115.5; DB 10;
81.1%; Pred. No. 7.2e-160;
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                                                                                                              EMBL; AF016459; AAD04199.1; -.
HSSP; P37821; 1B8G.
InterPro; IPR001176; ACC_synthase.
InterPro; IPR001511; Aminotran_1.
Pfam; PF00155; aminotran_1.2; 1.
PRINTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            487
                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 394; Conservative
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                                                                                                AMINOTRANSFERASES
                                                                                                                                                                                                                                                                               Pyridoxal phosphate. SEQUENCE 487 AA;
                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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NCBI_TaxID=3750;
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481 PLVKAT 486
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Geraniales; Geraniaceae; Pelargonium.
NCBL_TaxID=4031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSG 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALQRIRNFVLQNKEVVV -- SNKKHCWHSNL-RLSLKTRRFDDIT---MSPHSPLPQSPMV 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Pred. No. 1.8e-144; 68; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001176; ACC_synthase.
InterPro; IPR00151; Aminotran_1
PRO90155; aminotran_1_2; 1.
PRINTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.1%; Score 1922; 73.3%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U88971; AAB70885.1; -. HSSP; P37821; 1B8G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 75.1%
Best Local Similarity 73.3%
Matches 354; Conservative
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                                                                                                         SEQUENCE FROM N.A.
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  Sunako T., Ishikawa R., Senda M., Akada S., Niizeki M., Harada T.; "MdAGS-5A (Accession No. AB034992) and 5B (Accession No. AB034993), two wound-responsive genes encoding 1-aminocyclopropane-1-carboxylate synthase in apple. (PGR00-030)."; Plant Physiol. 122:620-620(2000).
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SUBUNIT: HOWODIMER (BY SIMILARITY).
-!- MISCELLANBOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
-!- SIMILARITY: BELOMGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 YAATVFSQPGFISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 CARKMSSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQ
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                                                                                                                                                                                                                                                                                                                                                                                          487 AA; 54648 MW; D23BEFCB1C68794F CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1-AMINGCYCLOPROPANE-1-CARBOXYLARE SYMTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.0%; Score 1945; DB 10;
73.4%; Pred. No. 2.6e-146;
11ve 63; Mismatches 59;
                                                                                                                                                                                                                                                              InterPro; IPR001176; ACC_synthase.
InterPro; IPR001511; Aminotran_1.
Pfam; PF00155; aminotran_1.2; 1.
PRINTS; PR00753; ACCSYNTHASE.
PNSOITE; PS00105; AA_TRANSFER_CLASS_1; 1.
Pyridoxal phosphate.
SEQUENCE 487 AA; 54648 MW; D23BEFCBIC
                                                                                                                                                                                                                            EMBL; AB034993; BAA92351.1; -. HSSP; P37821; 1B8G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359; Conservative
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Pelargonium hortorum.
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479 PQSPLVRAT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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P93772;
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Matches
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                                                                                                                                                            SUDAKOTT, ISHIKAWA R., Senda M., Akada S., Nilzeki M., Harada T.;
SUDAKOTT, ISHIKAWA R., Senda M., Akada S., Nilzeki M., Harada T.;
MAGAS-5A (Accession No. AB034992) and 5B (Accession No. AB034993),
TWO WOUND TESPONSIVE Genes encoding 1-aminocyclopropane-1-carboxylate
TWO WOUND TESPONSIVE GENES ENCODING TO THE PHYSIOL 122:650-620(2000).
TO FLAIL PHYSIOL 122:650-620(2000).
THE COPACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
THE SUBUNIT: HOMODIMER (BY SIMILARITY).
THE SUBUNIT: BELONGS IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC
ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
THE STATILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
EMBL; AB034992; BAA92350.1; -.
AMINOTRANSFERASES.
THE PRO01176; ACC_Synthase.
InterPro: IPR001176; ACC_Synthase.
InterPro: IPR001176; ACC_Synthase.
InterPro: PR001155; aminotran_1.
RR PRINTS: PR00153; aminotran_1.
RR PRINTS: PR00153; AM_TRANSFER_CLASS_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malus domestica (Apple) (Malus sylvestris).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids 1; Rosales; Rosaceae; Maloideae; Malus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLVEDWILNNPEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIVMSGGATGAHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIKEALEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARKMSSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQ 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DMAVQIALQRIRNFVLQNKEVVVSNKKH-CWHSNLRLSLKTRRFDDI-----TMSPHSPL 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SNAGLEVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMD
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8
                                                                                                                                                                                                                                                                                                                                                                                                                             Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                        54876 MW; 3E989EF2FBA73368 CRC64;
                      (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 1913; DB 10;
; Pred. No. 9.1e-144;
59; Mismatches 66;
  487 AA
                                                          1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                          74.8%;
72.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 356; Conservative
 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                             Pyridoxal phosphate. SEQUENCE 487 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                              NCBI_TaxID=3750;
                       01-OCT-2000
                                   01-OCT-2000
                                              01-DEC-2001
                                                                     MDACS-5A.
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local 9
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"Induction of ethylene and putrescine by ozone: Comparison of an ozone-sensitive and an ozone-tolerant hybrid popular clone."; ozone-sensitive and an ozone-tolerant hybrid popular clone."; submitted (ocr-1999) to the EmbLéenbank/DDBJ databases.
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT.
                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Malpighiales; Salicaceae; Populus.
NCBI_TaxID=75702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CV. I-45/51;
Koch J.R., Minocha R., Nakajima N., Yasutani I., Saji H., Rebbeck
Davis K.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 LLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDWILNN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                251 FISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMSSFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 VSTQTQYLLASMINDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQ-SNAGLFVWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71 PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3
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                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.5%; Score 1881.5; DB 10
73.5%; Pred. No. 2.9e-141;
11ve 58; Mismatches 65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB033502; BAA94599.1; --
HSSP; P371871, IBG.
InterPro; IPR001176; ACC_synthase.
InterPro; IPR00151; Aminotran_1.
PRAM; PF00155; aminotran_1.2; 1.
PRIWTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
                                                                                                                                  481
                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 349; Conservative
                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMINOTRANSFERASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pyridoxal phosphate.
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||||:|:||
479 PQSPLVRAT 487
                                                                                                                                                                                                                                                                                       Populus euphratica
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                                                                                                                                Q9MB76
Q9MB76;
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Query Match
Best Local Simi
Matches 347;
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                                                                                                                     Q9MB85
Q9MB85;
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                                                                                                                                                                                                                        367 DLSRLLKQQTFKAEMELWRVIIHEVKLNVSPGCSFHCLKPGWFRVCFANMDDETMQVALS 426
                                                                                                                                 Cucumis melo (Muskmelon).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSGGATG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIXSYNDAVVNCARKMSSFGL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 311 VSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTSDLVEDWILNN 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ishiki Y., Oda A., Yaegashi Y., Orihara Y., Arai T., Hirabayashi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVFSQPG
                 430 RIRNFVLQNKEVVVSNKKHCWHSNLRLSLKTRRFDDITMSPHSPLPQSPMVKATN 484
                           Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                            54904 MW; 95754805F958C8FB CRC64;
                                                                         O9FEM2 PRELIMINARY; PRT; 490 AA. O9FEM2; O1-MAR-2001 (TrEMBLrel. 16, Created) O1-MAR-2001 (TrEMBLrel. 16, Last sequence update) O1-DEC-2001 (TrEMBLrel. 19, Last annotation update) 1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE. CME-ACS2 (ME-ACS2).
                                                                                                                                                                                                                                                                                                                                                                                                                    73.3%; Score 1876; DB 10;
72.9%; Pred. No. 8e-141;
ive 62; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001176; ACC_synthase.
InterPro; IPR001511; Aminotran_1.
                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00155; aminotran_1_2; 1.
                                                                                                                                                                                                                                                                                                                         D86242; BAB18464.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                      347; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    phosphate.
                                                                                                                                                                                                                                                                                                                                                                                           490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                          PubMed-11074269;
                                                                                                                                                                                                   STRAIN-AMS
                                                                                                                                                                                                                                                                                                                                                                                    Pyridoxal
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SUBUNIT: HONODIMER (BY SIMILARITY).
-!- MISCELLANBOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cucumis melo (Muskmelon).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
LRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMDDMAVQIALQR 430
                                                                                             71 PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSGGATG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          431 IRNFVLQNKEVV--VSNKKHCW-HSNLRLSLKTRRFDDITMSPHSPLPQSPMVKAT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV. ANDES;
Shiom1 S., Yamamoto M., Inaba A.;
"Structural characterization of ACC synthase gene from melon and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..,
                                                                                                                                                                                            Length 490;
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                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Pred. No. 1.2e-140;
1; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                      490 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                      PRT;
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EMBL, AB032936; BAA93713.1; -.
HSSP; P37821; LBBG.
InterPro; IPR001176; ACC_synthase.
InterPro; IPR001511; Aminotran_1.
Pfam; PF00155; aminotran_1_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.2%;
ilarity 72.9%;
Conservative 61
                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=3659;
                                                                                                                                                                                                                                                  479 MVKA 482
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Submitted
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

ANDOR W.S., NIDGE W., Xu P.L., L1 N., Yang S.F.;

U.S., Wing W., Xu P.L., L1 N., Yang S.F.;

SUBMITCH (NOV-1998) to the EMBL/GenBank/DDBJ databases.

T. Colling-inducible ethylene blosynthesis in citrus plant.";

Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

T. CONTONE PRINCARL PHOSPHATE (BY SIMILARITY).

T. SUBMIT: HOMODIMER (BY SIMILARITY).

T. SUBMIT: HOMODIMER (BY SIMILARITY).

T. SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT

SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT

T. SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT

SEMBL; AJ012550; CAB60721.1; -.

SEMBL; AJ012550; CAB60721.1; -.

SEMBL; AJ012550; CAB60721.1; -.

SEMBL; AJ01251: 1886.

SEMBL; AJ01251: AJ01251: AJ01251: AJ01251: AJ01251.1 AJ01251: AJ01251
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VSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD 370
              LRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANMDDMAVQIALQR 430
                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudloctyledons; core eudlocts; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.
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                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.2%; Score 1873.5; DB 10
71.3%; Pred. No. 1.2e-140;
ive 70; Mismatches 64;
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PRINTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                             Citrus sinensis (Sweet orange).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 73.2
Best Local Similarity 71.3
Matches 345; Conservative
                                                                                                                                                                                                                                                                  PRELIMINARY;
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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC ONE AND A MITOCHOMDRIAL ONE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=FRUIT;
Shlomi S., Yamamoto M., Ono T., Kakluchi K., Nakamoto J.,
Nakatsuka A., Kubo Y., Nakamura R., Inaba A., Imaseki H.;
"cDNA cloning of ACC synthase and ACC oxidase genes in cucumber fruit
and their differential expression by wounding and auxin.";
J. Jpn. Soc. Hort. Sci. 67:685-692(1998).
                                                                                                                                                                                                            419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            360 QSNAGLEVWMDLRQLLKKPTFDSETELWKVIIHEVKINVSPGYSFHCTEPGWFRVCYANM
                                                                                                                                                                                                                                               359 KSNAGLFLWMDLHHLLKEQTYEAMALWRVIINEVKLNVSPGSSFHCPNPGWFRVCFANM
                                                                                                                                                                                                                                                                                                                                DDMAVQIALQRIRNFVLQNKEVVVSNKKH-CWHSNLRLSLKTRRFDDITMSPHSPLPQSP
                                                                                                                                                                                                                                                                                                                                                                Cucumis sativus (Cucumber).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta.
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosic
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                        NCARKMSSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCL
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Shlomi S., Yamamoto M., Inaba A.;
"Structural characterization of ACC synthase gene from melon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998 (TTEMBLrel. 08, Created)
01-NOV-1998 (TTEMBLrel. 08, Last sequence update)
01-DEC-2001 (TTEMBLrel. 19, Last annotation update)
ACC SYNTHASE (1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE).
CS-ACS2.
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InterPro: IPR001176; ACC_synthase.
InterPro: IPR001511; Aminocran_1.
Pfan; PF00155; aminotran_1.2; 1.
PRINTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     489
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L; AB006804; BAA33375.1; -.
L; AB032938; BAA93715.1; -.
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SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudloctyledons; core eudlocts; Rosidae;
eurosids II; Brassicales; Caricaceae; Carica.
NCBI_TaxID=3649;
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                                   134
                                                                      131 AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY 190
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STRAIN-SUBSET; TISSUB-30% YELLOW FRUIT;
Neupane K.R., Mukatira U.T., Stiles J.I.;
"Cloning of Fruit-specific ACC Synthase and ACC Oxidase cDNAs From Papaya (Carica papaya L.) and Their Expression During Fruit
                                                                                                                                                                  PEASICTPEGINDFRAIANFQDYHGLAEFRNAVAKFMARTRGNRITFDPDRIVMSGGATG
                   EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVFSQPG
                                                                                                                                                                                                                         FISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMSSFGL
                                                                                                                                                                                                                                                                                                  VSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ripening.";
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001176; ACC_synthase.
InterPro; IPR00151; Aminotran_1.
PRIMTS; PR00155; aminotran_1.2; 1.
PRIMTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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01-MAY-1999 (TrEMBLrel.
01-MAY-1999 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
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les 339; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACC SYNTHASE
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Matches
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|||||||| :| :|| || |||||||||| ||||| PEASICTAQGAAEFRDYHGLAEFREAVAKFWGKVRRNRASFDPDRIVWSGGATG 129
                                                                                                                                                                                                            311 VSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD 370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicotiana tabacum (Common tobacco).
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
131 AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY
                                                                                                                                                                                        EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVFSQPG
                                                                                                                                                                                                                                                          FISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMSSFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRNFVLQNKEVVVSNKKHCWHSNLRLSLKTRRFDDIT-----MSPHSPLPQSPMVKA
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.1e-134;
; Mismatches 72;
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68.1%; Pred. No. 4.1e
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PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
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InterPro; IPR001176; ACC_synthase.
InterPro; IPR001511, Aminotran_1.
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SEQUENCE FROM N.A.
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Matches 329;
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AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY
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LE-ACS1B.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                   CARKMSSFGLVSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQ 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cucurbita maxima (Pumpkin) (Winter squash).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosida I; Cucurbitales; Cucurbitaceae; Cucurbita.
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DLVEDWILNNPEASICTPEGINDFRAIANFODYHGLAEFRNAVAKFMARTRGNRITFDPD
                                                                                                                                                                                  LTKEALEDAYEKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEI
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Pred. No. 1.2e-133;
; Mismatches 69; Indels 7;
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Last annotation update)
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(TrEMBLrel. 19, I
(TrEMBLrel. 19, I
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01-DEC-2001 (T
ACC SYNTHASE.
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VQA 481
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ISOZYMES: A CYTOPLASMIC
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Oetiker J.H., Olson D.C., Shiu O.Y., Yang S.F.;

Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.

-1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE = 1-

AMINOCYCLOPROPANE-1-CARBOXYLARE + METHYLMIOADENOSINE.

-1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

-1- SUBUNIT: HOMODIMER (BY SIMILARITY).

-1- MISCELLANGOUS: IN BUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASM ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).

-1- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterida I; Solanales; Solanaceae; Solanum.

NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIRNFVLONKEVV -- VSNKKHCW-HSNLRLSLKTRRFDDITMSPHSPLPQSPMVKAT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   311 VSTQTQYLLASMLNDDEFVERFLAESAKRLAQRFRVFTGGLAKVGIKCLQSNAGLFVWMD
                                                                                                                                                                                                                                                                                                                                                                                         EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVFSOPG
                                                                                                                                                                      FISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMSSFGL
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE (EC 4.4.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-CV. RUTGERS;
Oono I., Nguyen M.D., Hennig L., Yu G., Rottoman W.H., C
Lincoln J.E., Theologis A.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> L.
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55E681096DDD7DC2 CRC64;
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1, U72390; AAB17279.1; -.
1, U74460; AAC49683.1; -.
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(TrEMBLrel. 02, I
(TrEMBLrel. 19, I
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Length 483;

10; B

Score 1781.5;

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'n,
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Lee Y.K., Lee S.H.;

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

-!- SUBUNIT: HOMODIMER (BY SIMILARITY).

-!- MISCELLANEOUS: IN EUKARYOTES THERE ARE TWO ISOZYMES: A CYTOPLASMIC ONE AND A MITOCHONDRIAL ONE (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO CLASS-I OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.
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                                                                                                                                                                131 AHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFVLTKEALEDAY 190
                                                                                                                                                                                                                        EKAREDNIRVKGLLITNPSNPLGTIMDRKTLRTVVSFINEKRIHLVCDEIYAATVFSQPG 250
                                                                                                                                                                                                                                                                             FISIAEILEDETDIECDRNLVHIVYSLSKDMGFPGFRVGIIYSYNDAVVNCARKMSSFGL 310
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                                                                   Gaps
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Micotiana glutinosa (Tobacco).

Micotiana ylutinosa (Tobacco).

Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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                           Indels
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Last annotation update)
        Pred. No. 2.6e-133;
6: Mismatches 65;
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HSSP; P37821; 1B8G.
InterPro; IPR001176; ACC_synthase.
InterPro; IPR001511; Aminotran_1.
Pfam; PF00155; aminotran_1.2; 1.
PRINTS; PR00753; ACCSYNTHASE.
PROSTIE; PS00105; AA_TRANSFER_CLASS_1; 1.
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69.18; Pt.
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                          327; Conservative
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SEQUENCE 482 AA;
           Best Local Similarity
Matches 327; Conserv
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                         59
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                                                                                                         RIVMSGGATGAHEVTAFCLADPGEAFLVPIPYYPGFDRDLRWRTGVKLVPVMCDSSNNFV
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MGFKAMDQTPLLSKMAIGDGHGESSPYFDGWKAYDQNPFHPTDNPNGVMQMGLAENQLTS
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MVQA 480
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Search completed: August 21, 2002, 02:11:26 Job time: 196 sec

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Gaps

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Indels

69.6%; Score 1781; DB 10; 68.6%; Pred. No. 2.8e-133; ive 74; Mismatches 72;

Query Match 69.6 Best Local Similarity 68.6 Matches 332; Conservative

Length 482;

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18 109.4 4.4 994 12 CNSOGNAGE	RESULT 1 CNSODEVL 1101 bp DNA linear GSS 04-JUN-1999 DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC: BACRESSION SERVEY sequence. ALG69706.1 G1:4949849 ALG69706.1 G1:4949849 KEYWORDS FILL FLY SOURCE ORGANISM Drosophila melanogaster ELWARYOTA: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; ELWARYOTA: Metazoa; Arthropoda; Tracheata; Brachycera; Muscomorpha; Ephydroidea; Drosophila. REFERENCE I (bases 1 to 1101) ALG69706.2 Genoscope. TITLE Direct Submission JOURNAL Submitted (02-JUN-1999) Genoscope. Centre National de Sequencage: When you senoscope. TITLE Submitted (02-JUN-1999) Genoscope. Centre National de Sequencage: When you senoscope. TITLE Submitted (02-JUN-1999) Genoscope. Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web. : www.genoscope.cns.fr - Web. : www.genoscope.cns.fr - Web. : www.genoscope.cns.fr - Web. : www.genoscope.cns.fr - Gelaboration of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).	melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: nbw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm. PEATURES
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM nucleic search, using sw model Run on: August 21, 2002, 00:26:04; Search time 3456.34 Seconds (without alignments) 9660.932 Million cell updates/sec 2474 Sequence: 14cacagatacacagaatcagtaaccacatacaccatagg 2474 Scoring table: IDENTITY_NUC Gapop 10.0, Gapext 1.0 Searched: 13736207 seqs, 6748477542 residues Total number of hits satisfying chosen parameters: 70tal number of hits satisfying chosen parameters: Minimum DB seq length: 000000000 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Listing first 45 summaries.	Database: EST:* 1: em_estba:* 2: em_estbum:* 3: em_esttin:* 4: em_estpi:* 5: em_estpi:* 5: em_estpi:* 6: em_estpi:* 10: qb_esti:* 11: qb_htc:* 12: qb_ess:* 13: em_gss_in=* 14: em_gss_in=* 15: em_gss_ln=* 15: em_gss_ln=* 16: em_gss_ln=* 16: em_gss_ln=* 17: em_gss_ln=* 18: em_gss_ln=* 18: em_gss_ln=* 19: em_gss_ln=* 19: em_gss_ln=* 10: qb_qss_ln=* 1	132 5.3 1101 12 CNSOGEVL ALO69706 Drosophil ALO69706 5.3 1101 12 CNSOGEVL ALO69706 Drosophil C

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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
   191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                   /organ1sm="Drosophila melanogaster"
/db_xref="taxon:7227"
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/clone="BACR29R72"
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster genome survey sequence T7 end of BAC: BAC259E3 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
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                                                                                                                               4;
                                                                                              Length 1101;
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Matches 226; Conservative 129; Mismatches 261;
                                                                                              Score 132; DB 12;
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/clone="BACR29B23"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1101;
DB 12;
              ilarity 38.1%; Pred. No. 8.8e-07;
Conservative 122; Mismatches 266
 5.3%; Score 130.6; 38.1%; Pred. No. 8.8
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Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                                                             Length 1152;
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                                                                             DB 10;
                                                                        Score 122.2; DB 10;
Pred. No. 8.3e-06;
0; Mismatches 437;
                                                                        Query Match
Best Local Similarity 47.0%;
Matches 392; Conservative
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1 (bases 1 to 1152)

8 Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton, R.D., Oates, R. and Main, D.

1 (Daylopment of a genetically and physically anchored EST resource for barley genomics: Morex unstressed seedling shoot cDNA library unpublished (2001)

1 (D) Feb 22, 2001 this sequence version replaced gi:13109934.

2 (Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Vector: lambdaZAP; Site_1: ECOR1; Site_2: Xhol; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedling shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give paluescript SK(·) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates , Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phreparation and sequence analysis see
                                                                                                                                         BG309087
HVSMEc0002a15f Hordeum vulgare seedling shoot EST 1brary
HVcDNA0003 (Etiolated and unstressed) Hordeum vulgare cDNA clone
HVSMEc0002a15f, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Hordeum vulgare seedling shoot EST library
HVCNNA003 (Etiolated and unstressed)"
//tissue_type="Seedling shoot"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
500 TTTTTWATTWATAWTTTWTTTWWANATTWWKKKK 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEC0002A15f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 13
High quality sequence stop: 1088.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
Total hq bases = 119
                                                                                                                                                                                                                                                                        BG309087.2 GI:16313791
                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare
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us-09-763-957-3.rst

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Lubrited (02-JUN-1999) Genoscope - Centre National de Sequencage : Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr )
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutcyo Osocgawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: n bw sp, the same strain used for the BDGP's pland EST libraries. A more detailed description of the library produced by the Labrary pland Experience of the library produced by the same strain used for the BDGP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genome survey sequence TET3 end of BAC: BACR29P01 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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  1685 atatatattaatttotttgaatatottttatacaagtaggtagactagaagaattatott 1744
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                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/db_xref="taxon:7227"
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/clone="BACR29P01"
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66 c 104 g
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- Web : www.genoscope.cns.fr)

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isogenic strain y2; on bw sp, the same strain used for the BDGF P1 and EST libraries. A more detailed description of the librar and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can k found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                      /organism="Drosophila melanogaster"
/db_xref="Laxon:7227"
/clone_lib="RPCI-98"
/clone="BACR29P01"
                                                                                                                                                                                                                                                                                                                                                                  DB 12;
                                                                                                                                                                                                                                                                                                                                                             4.7%; Score 117.4; DB 12;
10.3%; Pred. No. 3.1e-05;
Lve 93; Mismatches 277;
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66 c 104 g
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1296 tatgactcacattgtgttgatagggtgattttgtcaaaatatatgtctattttatactag 1355
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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                                                                                                                                                                                                     - Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Web: www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ilbrary was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The ilbrary is named RPCI-98 and was constructed by partial EcoRI digestion of Inosophila DNA provided by the BDGP from the isogenic strain v2: nbw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                 Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr
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                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterrygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilldae; Drosophila.
1 (bases 1 to 1101)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-and sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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1 (bases 1 to 1190)

Soset-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Weissenbach, J., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
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Seet-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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                                                                                                                                                    tattigtagatgitaaaigtaacgggcttagactgatgittitgiattatatattata 1814
1696 tttctt-tgaatatcttttatacaagtaggtagactagaagaattatcttatctcccgta 1754
                                                                                                                                                                                                                                                                                                                                                                                 500 AAWTAAAWAAAAAAAATTTTTTTTTTTTWAWTAAAWWTAWTWTTTTWTTTWWAATTT 441
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                                        620 KWDWKTRADRWDKWAADTWTDARKADRDWAKARAWRARRDRARAARADRRWTTKGKTTTA
                                                                                                                                                                                             Length 1190;
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/organism="Tetraodon nigroviridis"
/b_xref="taxon:99883"
/clone="153P04"
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CNSOOLT2 1101 bp DNA linear GSS 14-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC:
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/db_xref="taxon:7227"
                                                                                                  /clone_lib="RPCI-98"
/clone="BACR05N11"
/note="end : TET3"
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Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitily.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
Econt digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
Pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                        tatgatttgtctgcgaattatatatagtattaacttggagaaatgattgcctaataagtt 1415
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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AL061936.1 GI:4940214
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Drosophila melanogaster
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COMMENT

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Justice Jubilization

Submitted (11-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.cns.fr - Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutovyo Oscogawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the 1sogenic strain v2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://dacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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Best Local Similarity 35.8%; Pred. No. 0.00011;
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              fly), genomic survey sequence.
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Direct Submission
3ACR48P19
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Direct Submission

L Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cramelaux, CP 5706, 91057 EWYs cedex, FRANCE. (E-mail:
2 rue Gaston Cramelaux, CP 5706, 91057 EWYs cedex, FRANCE. (E-mail:
3 seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces Kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Varrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
Booltin-Fukuhara,M., Bon,E., Bortier,P., Casaregola,S.,
de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Liorente,B.,
Malpertuy,A., Neuvegilse,C., Ozier-Kalogeropoulos,O., Potier,S.,
Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
Wincker,P. and Weissenbach,J.
Genomic exploration of the hemiascomycetous yeasts: 1. A set of
yeast species for molecular evolution studies
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/db_xref="taxon:27293"
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Determination of this BAC-end sequence was carried out as part of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genome survey sequence SP6 end of BAC
BACNO1007 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL097152.1 GI:5608763
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone="ATOAA005D05"
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/note="end : T3"
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collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector peelobacil.
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/clone="BACN01007"
/note="end : SP6"
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR08K08"
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This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetracodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetracodon.
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Tetraodon nigroviridis.

Tetraodon nigroviridis.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontidae; Tetraodon.

1 (bases 1 to 994)

1 (bases 1 to 994)

1 (bases 1 to 994)

1 Neost-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetler, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Bernot, A., Elzames, C., Wincker, P., Brottier, P., Quetier, F., Burin, M. and Weissenbach, J. Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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t    172 others
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/db_xref-"taxon:99883"
/clone-"122P04"
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User Submitter (12-710/1999) Genoscope - Centre National de Sequencage : Direct Submitted (12-710/1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVAY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.cns.fr - General and the sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BAGs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammosor in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPGT-98 and was constructed by partial ECORI disestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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I (bases 1 to 1101)
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Bolotin-Fukuhara, M., Bon, E., Brottier, P., Casaregola, S.,
de-Wontigny, J., Dujon, B., Durrens, P., Lepingle, A., Llorente, B.,
Malpertu, A., Neuveglise, C., Ozier-Kalogeropoulos, O., Potier, S.,
Sautin, W., Tekaia, F., Toffano Nioche, C., Wesolowski-Louvel, M.,
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Duchateau-Nguyen,G., Lemaire,M., Marmeisse,R., Montrocher,R.,
Robert,C., Termier,M., Wincker,P. and Wesolowski-Louvel,M.
Genomic exploration of the hemiascomycetous yeasts: 11.
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Similarity 40.88;
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Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage,
2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail:
seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
This GSS is part of a random genomic sequencing program of thirteen
yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
angusta, Debaryomyces hansenii var. hansenii, Pichia sorbitophila,
Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
5 kb were prepared and both extremities were sequenced. See
keywords for description of this sequence and for the sequence of
the other extremity of this insert.
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?EBS Lett. 487 (1), 3-12 (2000)
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Search completed: August 21, 2002, 00:26:31 Job time: 5682 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM nucleic - nucleic search, using sw model	Run on: August 21, 2002, 01:59:05 ; Search time 96.17 Seconds (without alignments) 6318.990 Million cell updates/sec	Title: US-09-763-957-3 Perfect score: 2474 Sequence: 1 ttacagatacacagaatcagtaaccacatacaccatatgg 2474 Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 383533 seqs, 122816752 residues Total number of hits satisfying chosen parameters: 767066	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : Issued_patents_NA:* 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:* 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:* 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:* 4: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:* 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:* 6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES 8	Result Query No. Score Match Length DB ID Description	1 91.4 3.7 1511 1 US-07-991-867B-8 Sequence 2 91.4 3.7 1511 1 US-08-107-755A-8 Sequence 3 91.4 3.7 1511 2 US-08-544-332-8 Sequence	88.6 3.6 636 4 US-08-998-416-1137 Sequence 88.2 3.6 837 4 US-08-998-416-288 Sequence 88.2 3.6 19124 2 US-08-487-8268-13 Sequence	7 87.6 3.5 8920 2 US-08-446-855A-1 Sequence 8 87.6 3.5 8920 4 US-09-150-11 Sequence	83.4 3.4 615 4 05-08-09-08-05-08-08-08-08-08-08-08-08-08-08-08-08-08-	79.8 3.2 51952 3 US-08-998-416-186 Sequence 79.2 3.2 51952 3 US-08-947-823-1 Sequence	78.8 3.2 665 2 US-08-883-795A-36 78.6 3.2 6243 2 US-09-056-075-1 77.4 3.1 665 2 US-08-883-795A-36	74.4 3.0 6124 4 US-08-213-419B-3 Sequence 74 3.0 658 4 US-08-998-416-595 Sequence 73.4 3.0 1431 4 US-09-316-083-2 Sequence	21 73 3.0 3701 4 US-08-845-258-10 Sequence 22 73 3.0 3701 4 US-08-990-571-10 Sequence 23 73 3.0 3701 4 US-08-990-571-10 Sequence	72.8 2.9 6152 4 US-08-723-142A-10 Sequence 72.6 2.9 1431 4 US-09-316-083-2 Sequence 72.6 2.9 1431 4 US-09-316-083-2 Sequence 72.6 2.9 1431 1 US-08-32-463-14 Sequence	72.4 2.9 660 1 US-07-991-867B-32

Sequence 32, Appl	Sequence 32, Appl	Sequence 11, Appl	Sequence 15, Appl	Sequence 3, Appli	Sequence 305, App		Sequence 538, App		Sequence 534, App	Sequence 2, Appli		40,	• •	Sequence 40, Appl	3, A	40,	Sequence 305, App
US-08-107-755A-32	US-08-544-332-32	US-08-852-629-11	US-08-852-629-15	US-08-213-419B-3	US-08-998-416-305	US-08-998-416-595	US-08-998-416-538	us-09-056-075-1	US-08-998-416-534	US-07-867-106-2	US-08-845-258-3	US-08-845-258-40	US-08-990-571-3	US-08-990-571-40	US-08-723-142A-3	US-08-723-142A-40	US-08-998-416-305
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/08107755A
Patent No. 5721352
GENERATION:
GENERATION:
APPLICANT: Moyer: Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                       900 TATAATTTAAAAAAAATAATAATAAACAGAGATAATGTTATTAATATTAATAAAA
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compartible
COMPUTER: TBM PC compartible
COMPUTER: TBM PC compartible
COMPUTER: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/107,755A
FILING DATE: 19-AUG-1993
CLLASSIFICATION: 435
PRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/827,658
FILING DATE: 30-Jan-1992
PRICH APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAILMANCHIK, DAYIG R.
                                                                                                                                                                                                                                                                                                            1734 agaattatcttatctcccgtatatttgtagatgttaaat 1772
                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
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REGISTRATION NUMBER: 31,794
REPERENCE/DOCKET NUMBER: UF114.C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (904) 375-8100
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (18..218)
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EDNESS: double
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Pred. No. 9e-09;
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   Amsacta moorei entemopoxvirus
                                                                                                                   complement (234..782)
                                                           complement (18..218)
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Matches 501; Conservative
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852..1511
                                 NAME/KEY:
LOCATION:
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LOCATION:
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ORGANISM:
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US-07-991-8678-8
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1614 tcaatctattataatcatattagataaatatacaaatattgttaaattttacattat 1673
                                                                                1020 ATTCCAGAAAATATTAAAAGTTTATATTTCAAATTTAAATATTATTAATTTTAAATTTT 1079
                                                                                                                                           1080 ATAACAAAATTAAAAATATAACATATTTAGATATATCTTATAACAAAATAGCAATATA 1139
                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: MOYER, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Gerard H. Bencen
                                                                                                             tatattactaaatatattaatttetttgaatatetttatacaagtaggtagactaga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
                                                                                                                                                                           agaattatcttatctcccgtatattttgtagatgttaaat 1772
                                                                                                                                                                                               1140 AGTAATATTATACTACCACATTCTATAGAATTTTTAAAT 1178
                                                                                                                                                                                                                                                                                                                                                                                                         STREET: Gerard H. Bencen STREET: 2421 N.W. 41st Street, Suite A-1 CITY: Gainsville STATE: FL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Amsacta moorei entemopoxvirus
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CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION UNDER: US 07/991,867
FILING DATE: 07-DEC-1992
PRICH APPLICATION UNDER: US 08/107,755
FILING DATE: 19-AUG-1993
PRICH APPLICATION DATA:
APPLICATION UNDER: WO 92/14818
APPLICATION UNDER: WO 92/14818
APPLICATION UNDER: NO 92/14818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UF114.C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08544332
Patent No. 5935777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35,746
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REGISTRATION NUMBER: 35,746
REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 12-FEB 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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EDNESS: double
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OPERATING SYSTEM
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                                                                                                                              Length 1511;
                                                                                                                            Query Match 3.7%; Score 91.4; DB 1; Length 1!
Best Local Similarity 44.8%; Pred. No. 9e-09;
Matches 501; Conservative 0; Mismatches 596; Indels
                   complement (234..782)
                                                 CDS
852..1511
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; LOCATION:
; FEATURE:
; NAME/KEY:
; LOCATION:
US-08-107-755A-8
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ORIGINAL SOURCE:
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                                                                                                                                                                  Length 1511;
                                                                                                                                                                                          Indels
                                                                                                                                                               Score 91.4; DB 2;
Pred. No. 9e-09;
0; Mismatches 596;
                                                                    complement (234..782)
                            complement (18..218)
                                                                                                                                                               3.78;
                                                                                                                                                              Query Match
Best Local Similarity 44.8'
Matches 501; Conservative
                                                                                            CDS
852..1511
                                                      CDS
FEATURE:
NAME/KEY:
LOCATION:
                                                    NAME/KEY:
LOCATION:
                                                                                                         ; LOCATION:
US-08-544-332-8
                                                                                            NAME/KEY:
                                         FEATURE:
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APPLICANT: Poblmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Wendland, Jurgen
APPLICANT: Wendland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORRENT APPLCATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: MALGS J TIMOCHY
NAME: NAME: MALGS J TIMOCHY
REGISTRATION NUMBER: 38,415
ACCOUNTY OF TIMOCHY
NAME: MALGS J TIMOCHY
NAME: MALGS J TIMOCHY
REGISTRATION NUMBER: 38,415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSEE: No. 6233264artis Corporation
T: 3054 Cornwallis Road
Research Triangle Park
X: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1137, Application US/08998416 Patent No. 6239264
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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US-08-998-416-1137
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APPLICANT: Philip
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APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 50.4%;
Matches 298; Conservative
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APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
                                                                                                                                                                                                                                      ; ORGANISM: PAG1241RP
US-08-998-416-288
                                                                                                                                                                                               linear
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Patent No. 639364
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Steiner, Sabine
APPLICANT: Mendland, Jurgen
APPLICANT: Mendland, Jurgen
APPLICANT: Mendland, Jurgen
APPLICANT: Mendland, Jurgen
APPLICANT: Rechtle, Philipp
APPLICANT: Rechtle, Philipp
APPLICANT: Rebischung, Cortinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                              3;
  Length 636;
                           0; Mismatches 234; Indels
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Pred. No. 2.6e-08;
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CITY: Research Triangle Park
STATE: No. 6239264th Carolina
 3.6%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
Query Match 3.6
Best Local Similarity 51.5
Matches 252; Conservative
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US-08-998-416-288/c
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NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Pred. No. 3.2e-08;
0; Mismatches 283;
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; Patent No. 5993827
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1175 TGCATTATTACATAACATAACAAATAATTAATTACTATATATATATTTTTAATTATAT 1116
                                         caattaattagttgtgaattgatgacaaatatttcatgagcataaccaatcagagaaata 1130
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; Patent No. 5849573
; GENERAL INFORMATION:
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APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
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llarity 43.6%; Pred. No. 4.7e-08;
Conservative 0; Mismatches 743; Indels 5;
                                                                                                                                                                                                                                                                                          COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.25
                                                                                                                                         AUDRESSEE: Knobbe Martens Olson & Bear STREET: 620 Newport Center Drive 16th Floor CITY: Newport Beach STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: ISTACLSON NUMBER: 29,655
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121,001CP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: SINGle
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APPLICATION NUMBER: US/08/487,826B
FILLIG DATE: 10-SEP-1993
CLASSIFICATION: 435
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Best Local Similarity
Matches 579; Conserv
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                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                 444 TACACATCAAAATAATTAATTGTATTCATATTAATTGGAAATATTTAATAAGTTTTA 385
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APPLICANT: Stewart et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996
TITLE OF INVENTION: Synthetase II
FILE REFERENCE:
                                                                                                                                                                         tagtataaggagtctagaataaatttcttaaatattagaggaaaactattttaaaaaat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-12-02
EARLIER FILING DATE: 1993-12-06
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
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US-09-150-741-1/c
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... cLICANT: O'Sullivan, William J
TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl
TITLE OF INVENTION: phosphate synthetase II
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSE: Nixon ...
                                                                                                                                                             ADDRESSEE: Nixon & Vanderhye PC
STREET: 1100 No. 5849573th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
                                                                                                                                                                                                                                                                          COMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,855A
FILING DATE: 06-Jul-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47-80
RELECOMMUNICATION INFORMATION:
TELEPRANC 703-816-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8220 base_pairs
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384 TATTTCAAGTAATTTT------ATAAACAAATGAACACACAAACATATATATA 338
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APPLICANT: Sin, Kin L.
APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Miller, Louis H.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
ADDRESSEE: Robbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STREET: California
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                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 84.2; DB 2; Pred. No. 2.5e-07; 0; Mismatches 488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
Sequence 13, Application US/08487826B Patent No. 5993827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: ISraelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/POCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.48;
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TYPE: nucleic acid
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Matches 424; Conservative
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                                       GENERAL INFORMATION:
APPLICANT: Sim, K
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US-08-487-826B-13
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APPLICANT: Steiner, Sabine
APPLICANT: Wendrer, Sabine
APPLICANT: Wendland, Jurgen
APPLICANT: Wenchile, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TRY PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
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Patent No. 6299264
GEBERAL INFORMATION:
APPLICANT: Philippsen, Peter
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US-08-998-416-186/c
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Pred. No. 2.4e-07;
0; Mismatches 241;
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Patent No. 6239264
GENERAL INFORMATION:
                                                             CH 0016/97
               CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/9;
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: MALSO: J. TIMOCHY
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5:
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYRE: NUCLEIC acid
STRANDEDRESS: SING1E
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APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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24 - DEC - 1997
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Best Local Similarity 49.7
Matches 239; Conservative
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1830 taagttaatgtctcttttgattttaacatggttctaaaaattaggtttaatcattgcgt 1889
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   1770 aatgtaacgggcttagactgatgtttttgtattattattttataaatccattagagatt 1829
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APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Rechile, Philipp
APPLICANT: Rebischud, Corinne
TITLE OF INVENTION: GENOWIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Corwalls Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                           1950 totgagattgctcttaggattgaaattatgtttgatactagaaaacgaagaa 2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY AGENT INFORMATION:
REGISTRATION NUMBER: PF/5-30306/
REGISTRATION NUMBER: PF/5-30306/
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                             RESULT 12
US-08-998-416-186
; Sequence 186, Application US/08998416
; Detent No. 6239264
; GENERAL INFORMATION:
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Pohlmann, Rainer
Steiner, Sabine
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LENGTH: 615 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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MOLECULE TYPE: 1
ORIGINAL SOURCE:
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Pred. No. 5.1e-07;
0; Mismatches 279; Indels 12; Gaps
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                                                 APPLICANT: Reblachung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
UNMBER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                              COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RAPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF/5-30306/A/CCC1976
                                                                                                                                             SSEE: NO. 6233264artis Corporation
F: 3054 Cornwallis Road
Research Triangle Park
R: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
TELEFAX: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ 1D NO: 1137: SEQUENCE CHARACTERISTICS: LENGTH: 636 base pairs TYPE: nucleic acid STRANDEDNESS: $ingle
Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
ORIGINAL SURCE:
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50.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 3.3%
Best Local Similarity 50.8%
Matches 301; Conservative
                                                                                                                                                                                                          STATE: NO. COUNTRY: US. ZIP: 27709
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US-08-998-416-1137
                                                                                                                                                       ADDRESSEE:
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US-08-998-416-288
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US-08-947-823-1
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                                                      1470 ataataaaaaaacattatataagagattaagataatttaataagtattgaatgtagaataa 1529
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                                                                                                                                                                                                                                                        TTAATATG----AATACTATTTAGTCTATGTTCAAATTTTAAATTAGTTATTAAAATTT 253
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                                                                                                                                              20 TAATTTATAAAGATTAATATAAACTTTTTTATTATAATATTTAAGTATTAAATTTATAA
                                                                                                                                                                            aattcatcattcaatacgagtaattcaatctattataatcatattagataaatataca
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APPLICANT: Poblmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Knechtle, Philipp
APPLICANT: Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWHARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: US/08/998,416
FILING DATE: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6239264art1s Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 288, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-998-416-288
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1470 ataataaaaaacattatataaagagattaagataatttaataagtattgaatgtagaataa 1529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79.8; DB 4; Pred. No. 1.1e-06; 0; Mismatches 302;
                                                                                                                                               PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tagtgtatacacgtgtaaaaaaata 2036
PRIOR APPLICATION DATA:

APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38, 241
REFERENCE/DOCKET NUMBER: PF/5-303
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 288:
SEQUENCE CHARACTERISTICS:
LENGTH: 837 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   608 TAAAGAATGTAGTTAAAAATACTTATA 634
                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.2
Best Local Similarity 49.9
Matches 313; Conservative
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32622 TATTTGTTACAGAATATGACCACTAAATTC-GTATCTTCATTATTGAAATAATCTTTAAA 32680
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                              gaaggggttgatgacttcagctttaaaaataattcaactaaagttctagactacattggag 1004
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Sequence 36, Application US/O8883795A

Patent No. 5985607

GENERAL INFORMATION:

APPLICANT: Delcuve, Genevieve

APPLICANT: Awang, Gregor

TITLE OF INVENTION: Recombinant DNA Molecules and Expression

TITLE OF INVENTION: Vectors for Tissue Plasminogen Activator

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:
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Pred. No. 2.3e-06;
0; Mismatches 623; Indels 19; Gaps
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                                                            APPLICANT: Williamson, Valerie M.
APPLICANT: Kaloshian, Isgouhi
APPLICANT: Kaloshian, Jafar
APPLICANT: Yaghoobi, Jafar
APPLICANT: Bodeau, John
APPLICANT: Milligan, Stephen
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Post Resistance in Plants
TOWNER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                   COMPOTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                  E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 023070-070210US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/947,823
FILING DATE: US/08/947,823
CLASSIFICATION B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US97/18802
FILING DATE: 09-OCT-1997
PRIOR APPLICATION DATA:
FILING DATE: 105-OCT-1997
APPLICATION NUMBER: US 60/028,191
FILING DATE: 10-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BABELIAN, KEVIN L.
REGISTRATION UNDBER: 34,774
REFERENCE/DOCKET NUMBER: 0230
TELECOMMUNICATION INFORMATION:
TELEFONE: (415) 576-0200
ILEPERAX: (415) 576-0200
INFORMATION FOR SEQ ID NO: 1:
Sequence 1, Application US/08947823
Patent No. 6114605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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3.2%;
Best Local Similarity 45.3%;
Matches 532; Conservative 0
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LENGTH: 51952 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                          STREET: Two Embarcad
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                94111-3834
                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.2%; Score 78.8; DB 2; Length 66 Best Local Similarity 48.6%; Pred. No. 1.7e-06; Matches 246; Conservative 0; Mismatches 257; Indels
          STATE: 40 KING SIRECT WEST
CITY: TOCONTO
STATE: ONTAIO
COUNTRY: Canada
ZIP: MASH 3YZ
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN BATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 27-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gravelle, Micheline
REGISTRATION NUMBER: 7841-062
FELERAK: (416) 364-7311
TELEFAK: (416) 364-7311
TELECOMMULCATION INFORMATION:
TELEFAK: (416) 364-7311
TELEFAK: (416) 365-361
SEQUENCE CHARACTERISTICS:
LENGTH: 665 base pairs
TYPE: NUCLEIC acid
STRANDEDESS: SINGLE
TOCONCOTTE INCOME.
TYPE: Linear
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40 King Street West
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear

MOLECULE TYPE: CDNA

ORIGINAL SOURCE:
ORGANISM: Homo sapiens

INMEDIATE SOURCE:
CLONE: Rh 32
US-08-883-795A-36
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DD 527 TATTTATAATTACATATTTATAATT 552
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Search completed: August 21, 2002, 02:01:01 Job time: 9412 sec

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GenCore version 4.5 Copyright (c) 1993 – 2000 Compugen Ltd.	ic - nucleic search, using sw model	August 21, 2002, 02:07:21 ; Search time 477.34 Seconds (without alignments) 8898.576 Million cell updates/sec	US-09-763-957-3 score: 2474 :: 1 ttacagatacacagaatcagtaaccacatacaccatatgg 2474	table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	l: 1736436 seqs, 858457221 residues	mber of hits.satisfying chosen parameters: 3472872	DB seq length: 0 DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	N_Geneseq_032802:* SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:* 2: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:* 3: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:* 4: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1983.DAT:* 5: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1985.DAT:* 6: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1985.DAT:* 7: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1986.DAT:* 8: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:* 9: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:* 10: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:* 11: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT:* 12: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1991.DAT:* 13: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1991.DAT:* 14: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1992.DAT:* 15: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1995.DAT:* 16: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:* 17: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:* 18: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:* 19: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:* 19: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:* 20: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:* 21: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:* 22: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:* 23: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:* 24: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA20018.DAT:* 24: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA20018.DAT:* 24: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA20018.DAT:* 24: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA20018.DAT:* 24: /SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA20018.DAT:*
		Run on:	Title: Perfect score: Sequence:	Scoring table:	Searched:	Total number of	Minimum DB seq Maximum DB seq	Post-processing	Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Mung bean ACC synt	Human immune syste	Tumour suppressor	Human immune syste	Human immune syste	Tumour suppressor	Human metastasis a	Human inflammatory	Sequence of ANS-1
a	AA294266	ABL34155	AAS46429	ABL33472	ABL33307	AAS46287	ABL34493	AAH93026	AAN71405
DB	21	24	22	24	24	22	24	22	00
% Query Match Length DB ID	2474								
& Query Match	100.0	4.8	4.5	4.5	4.4	4.4	4.2	4.2	4.2
Score	2474	119.2	110.4	110.4	109.4	108.2	104.8	103.4	102.8
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	6	101	_	12393		ABL33263			immune syste
	4	100.6	٠.	1676		ABL34598			
(ח ע	8. G	9.0	6123		ABL32821			immune syste
ט	0 1	7 · 6 6		5000		ABL34133		Human	immune syste
	- @	66	. 0	7461		ABL33784			immine syste
	0	98.4	0	19787		ABL33451		Human	immune syste
	٥,	97.8	0,1	5979		AAS45313		Chemic	cally pretrea
C	- €	97.6		8305		ABL33569		Human	immune syste
י	23	97.4	, o.	6071	7 7	ABL32325		Human	immune syste
	4	97.4	6.	6071		AAS61076			
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บ	۰ ۵	8.90	ه ز.	17280		AAN6U4/2 AAS46771	••	Sequenc	യ
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	, o	96.4	۰۰	5413		AAS46694		Tumour	suppressor
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(- - (96.4	٥.	13584		ABL32615		Human	immune syste
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	٠ 4	4.56	. 0	61020		AAS45388		THE	The suppressor
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	. ~	94.2		5999		ABL32853			immune syste
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A C	AAZ94	4266;							
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DE	Mung	bean ACC	syntha	se	AIM-1	gene promoter pGEL	-1.		
XX									
M M	Mung	bean; 1	-aminocyc	ゖ	opropa	-1-carboxylic	d synthase;	7	
X	۲	ı yırıması,	416	יי בי בי		, poet-1; crand		.; ds.	
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XX PI	Botella	lla Mesa	JR,	Cazzonel	el11	CI;			
XX									
S S	WPI;	2000-270821	821/2	23.					
PT	Isol	solated nucleic acid molecule	eic	acid mo	lecu	for producing	ansgenic	c plant	s having
PT	altered	red chara	cteri	characteristics	such	s resistance to	plant p	pathoge	a plant pathogen
PŢ	COMP	comprises pro	promoter,	c, inducible	cibl	in response to	ysical	stimula	tion -

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The present sequence is that of the promoter, termed pGEL-1, of the mung bean 1-aninocyclopropane-1-carboxylic acid synthase gene, AIM-1.

AIM-1 was identified as a mechanical strain-induced gene, and the promoter was cloned using a long distance inversion PCR procedure.

PER-1 is capable of induction by physical and/or environmental of stimuli in cells in which it is indigenous and, in the absence of any negative regulatory mechanism, is capable of constitutive expression in cells in which it is non-indigenous. The invention captess to this promoter, and also to derivatives of the promoter including modular forms which are, for example, inducible by different physical and environmental stimuli or which are constitutively expressed. The promoter can be used to direct expression of genes conferring useful traits on plants, such as improved resistance to a plant pathogen, altered anititional characteristics, expression of a plant pathogen, altered blochemical pathway, altered fertility, and/or altered flower colour. English 41-11; 111pp; F1g Claim

Sequence 2474 BP; 844 A; 372 C; 363 G; 895 T; 0 other;

ö 300 300 360 gcgtgctgtcgaagaacacataattttgaggttgaagctcacgtgcgagttttgcatatt 420 420 480 480 tccatataccaattaatttattttttaatttatgcattttgatcttatattaaaacaatt 720 ggagattatggtacgacaagatgaaatgtttttatatggttgagattattttggtctgtt 120 Gaps ttacagatacacagaatcagacgacacatttactttaataacagaaaaataataagtgtc 60 atgttcatgcaactgttcttcgctaactaaggcccacttacctttataatattctctct atgitical generation to the sectangly of the section of the sectio aaaaaaccaaaagcaatagctactctgtaaggtcctcgattgccgacaagaacatcacat Length 2474; ö Indels DB 21; Ouery Match 100.0%; Score 2474; Best Local Similarity 100.0%; Pred. No. 0; Matches 2474; Conservative 0; Mismatches Н 9 121 241 481 541 61 121 181 181 241 301 301 361 361 421 421 481 501 601 661 g à 셤 ð g Q Q g g 셤 ç ŏ a ò 셤 å a δ à à ò å

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                                  gttctaaaaaattaggtttaatcattgcgtcctcaatgaacccatgctatatgttttaaag
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0; Mismatches 828;
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43.9%; Pred. No. 1e-
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                                                      2000DE-1032529.
2000DE-1043826.
02-JUL-2001; 2001WO-EP07537
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Best Local Similarity 43.9
Matches 651; Conservative
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01-SEP-2000;
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with blaulphile, of genes associated with fumour suppressaon and concogenes having a sequence taken ifrom 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences.

CG character acid-objagement (PNA) of at least 9 nucleotides and may be a complementary to (58). The nucleic acid may be a complementary to (58) and sequences complementary to (58). The nucleotides and may complementary to (58) and sequences complementary to (58). The nucleotides and may complementary for a set of probes for detecting the cytosine methylation state array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for a secretaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters in the compared to another set of genetic and/or epigenetic parameters and care disadvantageous to patients. The present sequence is one of the compared compared to another set of genetic methylations. The present sequence is one of the compared compared to another set of genetic methylations and compared to another set of genetic sequence is one of the concept and concept compared to another sequences derived from tumour suppressor genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
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cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
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0; Mismatches 691;
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4.5%; Score 110.4;
Best Local Similarity 45.1%; Pred. No. 1.9
Matches 579; Conservative 0; Mismatches
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2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                         cytosine methylation; ds.
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                                                                                                                                WO200168912-A2.
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30-JUN-2000;
01-SEP-2000;
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                                                                                        Homo sapiens
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzhemer's disease, Alzhemer's disease, Alzhemer's disease, Alzhemer's disease, and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                      antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhomatic; antiarthritic; antidabetic; antipsoriatic; antilnflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                            immune system disease; cytosine methylation; antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid comprising fragment of chemically modified gene, use for diagnosis and treatment of diseases associated with abnormal cytosine methylation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 1445; 32pp + Sequence Listing; German.
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Pred. No. 1.9e-07;
); Mismatches 691;
                                                                                                                                                                                              Human immune system associated gene SEQ ID NO:
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukeamia, Alzheimer's disease, AnDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
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suppressor
                                                                                                                                                                                                                                                        Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
cytosine methylation; ds.
tattgatatttgtttattttatattttatatttattttatatttgtattttatatttgtttac 5880
                    atgtctctctttgattttaacatggttctaaaaattaggtttaatcattgcgtcctcaat
                                      5941 taattatttagatatttatttgtatatttaaatgtttatatatattttgtttttatattt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fragments of chemically modified genes associated with tumour supp
genes and oncogenes, useful in designing primers and probes for
analysing diseases associated with cytosine methylation state e.g.
                                                            Tumour suppressor gene derived chemically modified sequence #9.
                                                                                                  1957 ttgctcttaggattgaaattatgtttgatactagaaa 1993
                                                                                                              Claim 1; SEQ ID No 9; 27pp; English.
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5287/c
AAS46287 standard; DNA; 8169
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06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1043826.
                                                                                                                                                                                                                                                                                                                                                             15-MAR-2001; 2001WO-EP02955
                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG.
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                                                                                                                                                                                                                                                                                                  Homo sapiens.
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The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with bisulphile, of genes associated with tumour suppression and concogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences complementary to (Ss). The nucleic acid may be as peptide nucleic acid-oligoment (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the

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                                                                                                        Score 108.2; DB 22; Length 8169;
Pred. No. 3.8e-07;
0; Mismatches 498; Indels 10;
genomic sequences derived from tumour suppressor genes and
                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                          Sequence 8169 BP; 2420 A; 116 C; 1665 G; 3960 T; 8 other;
                                                                                                           A.4%;
Similarity 46.8%;
                                                                                                                      Best Local Similarity 46.8
Matches 447; Conservative
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The present invention provides a number of human metastasis associated genes which are modifiled by cytosine methylation. The sequences can be used in the diagnosis and treatment of cancer. The present sequence is one of the genes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid derived from chemically treated metastasis genes, useful for diagnosis of cancers by analysis of cytosine methylation, also for treatment
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                    Sequence 11996 BP; 2966 A; 261 C; 3041 G; 5728 T; 0 other;
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                                                                                                                                                                                                                                                                                            cytostatic; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 24;
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Pred. No. 1.1e-06;
0; Mismatches 392;
                                                                                                                                                                                                                                                         Human metastasis associated gene SEQ ID NO: 46.
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                                                                                                                                    ABL34493 standard; DNA; 11996
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Best Local Similarity 47.9%;
Matches 365; Conservative 0
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2000DE-1032529.
2000DE-1043826.
                                                                                                                                                                                                                                                                                            Metastasis associated gene; cytosine methylation; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-APR-2001; 2001WO-EP03970
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                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                            WO200177376-A2.
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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colitis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ig for the presence of polymorphisms associated with inflammatory disease, using a hybridization assay -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forensic test; gene therapy; ds.
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                                               ttcaaagtaaataatagatataattcatcattcaatacgagtaattcaatctattataat
                                                                                                                                     cccgtatattttgtagatgttaaatgtaacgggcttagactgatgtttttgtattatatta
                                                                                                                                                                                                                           aattaggtttaatcattgcgtcctcaatgaacccatgctatatgttttaaagttttttgt
                                  taagtattgaatgtagaataatttttatttataaatttgaactaaaatattcaaataata
                                                                                                                        catatattagataaaatatacaaatatttgttaaattttacattattatattactaaatat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human inflammatory bowel disease related gene fragment IGR3319a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; inflammatory bowel disease; Crohn's disease; ulcerative
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ID AAH93026 standard; DNA; 700
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10-APR-2000;
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The present invention describes a method for detecting the presence of polymorphisms associated with inflammatory bowel diseases such as ulcerative colitis and Crohn's disease. The methods can be used to detect the presence of genetic polymorphisms associated with inflammatory bowel disease and correlating their occurrence with disease states. They may be used in this way for phenotypic correlations, forensics, patentity testing, medicine and genetic analysis. The present sequence is a gene containing a polymorphic site described in the exemplification of the
                                                                                                                                                                                                                  1273 tttaaattatctaacaattttcttatgactcacattgtgttgatagggtgattttgtcaa 1332
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                                                                                                                                                                                                                                                                                                                                                                         Enzyme; fungal expression vector; Aspergillus expression vector;
                                                                                                                                                                                            6
                                                                                                                                                                  Length 700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transformation efficiency.
                                                                                                                            Sequence 700 BP; 370 A; 13 C; 14 G; 302 T; 1 other;
                                                                                                                                                                  22;
                                                                                                                                                                Score 103.4; DB 22;
Pred. No. 2.1e-06;
0; Mismatches 292;
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llarity 50.5%;
Conservative
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Matches 307;
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1390 INAAGGICAANTATATITATATITTAATIAATIAATIAATINITIAGIATIANTAAG 1331
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                                                                                                                                                                                                                                                                                                                                                                            A DNA sequence coding for a heterologous polypeptide which can be expressed in and secreted from filamentous fungi is claimed. Pref. the DNA sequence codes for bovine preprochymosin, M. meihai preprocarboxyl protease or A. niger preproglucoamylase. Also new are vectors consisting of the DNA sequence plus an operably-linked signal sequence. The vectors may also include a sequence which increases transformation efficiency, e.g. ANS-1.
                                                                                                                                                                                                                                                                                  New DNA sequences for expressing polypeptide in filamentous fungi
- with secretion of prod. from the cells, and new vectors and
transformed fungi
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Pred. No. 2.4e-06;
0; Mismatches 793;
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Similarity 42.08;
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                                                                                                                                                                                                (GENE-) GENENCOR INC
                                                                                                                                                                                                                             Gray GL,
                                                                                                                                                                                                                                                           WPI; 1987-095049/14.
Trichoderma; ds.
                              Mucor miehei
                                                                                                                    27-AUG-1986;
                                                                                                                                                                 29-AUG-1985;
                                                                                                                                                  07-JUL-1986;
                                                                                      25-MAR-1987
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Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilia; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome;
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790 TAGGTATACTINITAATNITAAAAATITAATAATTITTIATATATAGAATAGTAAGG 731
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renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid sequences from chemically modified genes associated with gene regulation, useful for analysing cytosine methylations for diagnosis and therapy of diseases e.g. severe combined immunodeficiency
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2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG
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                                                                                                                                          WO200177375-A2
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The invention relates to 224 nucleic acid sequences comprising at least 18 bases of a chemically pretreated gene associated with gene regulation selected from 43 known genes (or complementary sequences). The chemical pretreatment converts of complementary sequences). The chemical pretreatment converts of complementary sequences). The chemical pretreatment converts of complementary sequences. The chemical pretreatment converts of complementarion methylated at the dispinant of cytosine methylations. The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene requisation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac alsorders, haemophilia, solid tumours and cancer, werner syndrome, sethma, HDR syndrome, Saethre-Chorcan syndrome, renal disease, preeclampsia, graft versus host disease. The present sequence is a ssociated with the human gene regulation-associated genes.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the very content directly from WIPO at 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Gene regulation-associated gene; severe combined immunodeficiency; cardiac damage; inflammatory response; Haemophilla; Werner syndrome; asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrome; renal disease, Preeclampsia; cardiac allograft vascular disease, colorectal cancer; thyroid cancer; coephageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic; nephrotropic; gynecological; anti-tumour; immunosuppressive; cytostatic.
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    3338 agigattatgittitaaagaaaaaatataaattititgitagigattagitatattiaat 3397
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                                                                                                                                                                                                                                                                                                                                                                                                                                 colitis;
                                                                                                                        Human; inflammatory bowel disease; Crohn's disease; ulcerative colitis single nucleotide polymorphism; SNP; chromosome 19p13; paternity test; chromosome 5q31-33; forensic test; gene therapy; ds.
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used in this way for phenotypic correlations, forensics, paternity testing, medicine and genetic analysis. The present sequence is a gene containing a polymorphic site described in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                           Sequence 700 BP; 370 A; 13 C; 14 G; 302 T; 1 other;
                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                           0; Mismatches 287;
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Pred. No. 4.1e-06;
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Similarity 52.1%;
3; Conservative
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neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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Pred. No. 3.8e-06;
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Matches 685; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                New nucleic acid derived from chemically treated metastasis genes, useful for diagnosis of cancers by analysis of cytosine methylation, also for treatment
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                                                                                                      cancer;
                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 151; 23pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7676 BP; 2396 A; 45 C; 1348 G; 3887 T; 0 other;
                                                                                            cytostatic; gene therapy;
ds.
                                                                                Human metastasis associated gene SEQ ID NO: 151
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                   ВР
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                 ABL34598 standard; DNA; 7676
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07-APR-2000; 2000DE-1019173.
30-JUN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
                                                                                                                                                                                              06-APR-2001; 2001WO-EP03970
                                                                                                     gene;
                                                                                                              cytosine methylation; gene;
                                                           (first entry)
                                                                                                                                                                                                                                                                                          Piepenbrock C,
                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG.
                                                                                                     associated
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                                                                                                                                                    WO200177376-A2
                                                                                                                                   Homo sapiens.
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                                      attcaactaaagttctagactacattggagattttagtgttcataaaattttagaaaaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gacaattgaagttttcctcaagtttagccatttttatgaaattaaacttaatcactacta 807
                                                                                                                                                                                                 antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirhemmatic; antiarthritic; antidabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal
                23;
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  aaataatagttgtgggaacttaagttggatttgaatactaggacgaggctgga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 794; 32pp + Sequence Listing; German.
                                                                                                                                                                                      Human; immune system disease; cytosine methylation;
                                                                                                                                                              Human immune system associated gene SEQ ID NO: 794.
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14.6%; Pred. No. 5.9e-06;
Lve 0; Mismatches 752;
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01-SEP-2000; 2000DE-1043826
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Matches 624; Conservative
                                                                                      DNA;
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                                                                                     ABL32821 standard;
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tcaat	-	aatag
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cattg	=	gttt
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